

List of potentially matching sequences

Send selected sequences to Clustal W (multiple alignment)Submit QuerySelect up to...☐ Include query sequence

Db AC	Description	Score	E-value
<input type="checkbox"/> sp P19196	INVA_YEREN <u>Invasin</u> <u>Yersinia enterocolitica</u>	1639	0.0
<input type="checkbox"/> tr Q56889	Invasin [invA] [Yersinia enterocolitica]	1613	0.0
<input type="checkbox"/> sp P11922	INVA_YERPS Invasin [Yersinia pseudotuberculosis]	726	0.0
<input type="checkbox"/> tr Q56937	Invasin [inv] [Yersinia pestis]	721	0.0
<input type="checkbox"/> tr Q8ZA73	Putative invasin (Hypothetical) [YPO3944] [Yersinia pe...	428	e-118
<input type="checkbox"/> tr Q74QZ6	Putative invasin [YP3306] [Yersinia pestis]	428	e-118
<input type="checkbox"/> tr Q6KC27	Intimin lambda <u>[eae]</u> [Escherichia coli]	342	2e-92
<input type="checkbox"/> tr Q8KRK8	Intimin lambda [Escherichia coli]	340	6e-92
<input type="checkbox"/> tr Q8VL95	Theta <u>intimin</u> [eae] [Escherichia coli]	336	1e-90
<input type="checkbox"/> tr Q8VL00	Theta intimin [Escherichia coli]	335	2e-90
<input type="checkbox"/> sp O31000	EAE_ECO11 Intimin (Attaching and effacing protein) (Ea...	333	6e-90
<input type="checkbox"/> tr Q6EV99	Intimin sigma [eae] [Escherichia coli]	332	2e-89
<input type="checkbox"/> tr Q93FK0	Intimin <u>[Citrobacter rodentium]</u>	331	3e-89
<input type="checkbox"/> tr Q93UI3	Intimin type gamma [eae] [Escherichia coli]	331	4e-89
<input type="checkbox"/> tr Q842D8	Intimin [eae] [Escherichia coli]	330	5e-89
<input type="checkbox"/> tr P77067	Beta intimin (Eae) [eaeA] [Escherichia coli]	330	5e-89
<input type="checkbox"/> tr Q9RCH1	Intimin [eaeA] [Escherichia coli]	330	7e-89
<input type="checkbox"/> tr Q9R8R5	Intimin [eae] [Escherichia coli]	330	7e-89
<input type="checkbox"/> tr Q9S6R2	<u>Intimin</u> [eaeA] [Escherichia coli]	330	7e-89
<input type="checkbox"/> tr Q6KC44	Intimin mu [eae] [Escherichia coli]	330	7e-89
<input type="checkbox"/> tr Q47018	Intimin [eaeA] [Escherichia coli]	330	9e-89
<input type="checkbox"/> tr Q8X6G3	Putative adhesin [eaeH] [Escherichia coli O157:H7]	329	1e-88
<input type="checkbox"/> tr Q93K93	Intimin-kappa [eae-kappa] [Escherichia coli]	329	1e-88
<input type="checkbox"/> tr Q7AHB0	Putative invasin [ECs0336] [Escherichia coli O157:H7]	329	1e-88
<input type="checkbox"/> tr Q8FKK3	Putative adhesin [eaeH] [Escherichia coli O6]	329	1e-88
<input type="checkbox"/> tr Q93K94	Intimin-jota [eae-jota] [Escherichia coli]	328	2e-88
<input type="checkbox"/> tr Q9LBG6	Intimin [eae] [Escherichia coli]	328	2e-88
<input type="checkbox"/> tr Q6KC43	Intimin nu [eae] [Escherichia coli]	328	2e-88
<input type="checkbox"/> tr Q8KRL1	Intimin epsilon 2 [Escherichia coli]	327	4e-88
<input type="checkbox"/> tr Q9EXN4	Intimin zeta [eae] [Escherichia coli]	326	1e-87
<input type="checkbox"/> tr Q8KRK9	Intimin beta 2 [eae] [Escherichia coli]	326	1e-87
<input type="checkbox"/> sp Q07591	<u>EAE</u> CITFR Intimin (Attaching and effacing protein) (Ea...	326	1e-87
<input type="checkbox"/> tr Q6QZW1	Eae~ (Fragment) [Escherichia coli]	326	1e-87
<input type="checkbox"/> tr Q6KC41	Intimin pi [eae] [Escherichia coli]	326	1e-87
<input type="checkbox"/> tr Q6KC42	Intimin xi [eae] [Escherichia coli]	325	2e-87
<input type="checkbox"/> tr Q8VL93	Zeta intimin [Escherichia coli]	325	2e-87

<input type="checkbox"/>	tr Q846P2	Intimin-zeta [eae] [Escherichia coli]	325	3e-87
<input type="checkbox"/>	sp P43261	EAE_ECO57 Intimin (Attaching and effacing protein) (Ea...	324	4e-87
<input type="checkbox"/>	tr Q9RGP3	Intimin type epsilon [eae] [Escherichia coli]	324	4e-87
<input type="checkbox"/>	tr Q9R8B5	Gamma intimin [eae] [Escherichia coli]	324	4e-87
<input type="checkbox"/>	tr Q9R8B4	Gamma intimin [eae] [Escherichia coli]	324	4e-87
<input type="checkbox"/>	tr Q8RSS9	Intimin eta [eae] [Escherichia coli]	323	1e-86
<input type="checkbox"/>	tr Q84FQ2	Intimin epsilon [Escherichia coli]	323	1e-86
<input type="checkbox"/>	tr Q93UI4	Intimin type beta [eae] [Escherichia coli]	322	2e-86
<input type="checkbox"/>	tr Q8RNT8	Intimine type epsilon [eae] [Escherichia coli]	322	2e-86
<input type="checkbox"/>	tr Q8KRL0	Intimin alpha 2 [eae] [Escherichia coli]	321	4e-86
<input type="checkbox"/>	tr O06896	Intimin [eae] [Escherichia coli]	318	2e-85
<input type="checkbox"/>	tr O52620	Intimin [eaeA] [Escherichia coli]	318	3e-85
<input type="checkbox"/>	sp P19809	EAE_ECO27 Intimin (Attaching and effacing protein) (Ea...	317	6e-85
<input type="checkbox"/>	tr Q9F609	Intimin type epsilon (Fragment) [eaeA] [Escherichia coli]	316	1e-84
<input type="checkbox"/>	tr Q8KRL2	Intimin jota 2 [Escherichia coli]	316	1e-84
<input type="checkbox"/>	tr Q6KAV7	Intimin rho [eae] [Escherichia coli]	311	2e-83
<input type="checkbox"/>	tr Q7N599	Similarities with putative adhesin [plu2057] [Photorha...	310	9e-83
<input type="checkbox"/>	tr Q9EYM6	Intimin type epsilon (Fragment) [eaeA] [Escherichia coli]	310	9e-83
<input type="checkbox"/>	tr Q8XB95	Putative invasin [z5932] [Escherichia coli O157:H7]	304	4e-81
<input type="checkbox"/>	tr Q7A8L6	Putative invasin [ECs5290] [Escherichia coli O157:H7]	298	4e-79
<input type="checkbox"/>	tr Q8D083	Putative adhesin [y2605] [Yersinia pestis]	296	1e-78
<input type="checkbox"/>	sp P76347	YEEJ_ECOLI Hypothetical protein yeeJ [yeeJ] [Escherich...	293	1e-77
<input type="checkbox"/>	sp Q8X8V7	YEEJ_ECO57 Hypothetical protein yeeJ [z3135] [Escheric...	289	2e-76
<input type="checkbox"/>	tr Q7CQ17	SinH [sinH] [Salmonella typhimurium]	245	3e-63
<input type="checkbox"/>	tr Q9XCI9	SinH [sinH] [Salmonella typhimurium]	245	3e-63
<input type="checkbox"/>	tr Q8FF61	SinH homolog [c3031] [Escherichia coli O6]	235	3e-60
<input type="checkbox"/>	tr Q9L574	Invasin-like SivH [sivH] [Salmonella typhi]	233	9e-60
<input type="checkbox"/>	tr Q7X2C2	Aec1 precursor [aec1] [Escherichia coli]	233	1e-59
<input type="checkbox"/>	sp P36943	EAEH_ECOLI Attaching and effacing protein homolog prec...	209	1e-52
<input type="checkbox"/>	sp P39165	YCHO_ECOLI Hypothetical protein ychO [ychO] [Escherich...	199	2e-49
<input type="checkbox"/>	tr Q8XDD4	YchP protein [ychP] [Escherichia coli O157:H7]	198	3e-49
<input type="checkbox"/>	tr Q7AEU6	Putative factor [ECs1725] [Escherichia coli O157:H7]	198	3e-49
<input type="checkbox"/>	tr Q83RN8	Putative factor [ychP] [Shigella flexneri]	198	4e-49
<input type="checkbox"/>	tr Q7UCS2	Putative factor [ychP] [Shigella flexneri]	198	4e-49
<input type="checkbox"/>	tr Q8FHZ3	Hypothetical protein ychP [ychP] [Escherichia coli O6]	195	3e-48
<input type="checkbox"/>	tr Q93GR3	Putative adhesin [PSLT034] [Salmonella typhimurium]	190	8e-47
<input type="checkbox"/>	tr Q8ZP33	Putative invasin [ychP] [Salmonella typhimurium]	186	1e-45
<input type="checkbox"/>	tr Q8Z7G3	Putative invasin [STY1284] [Salmonella typhi]	186	1e-45
<input type="checkbox"/>	tr Q8ZP78	Homology to invasin C of Yersinia; intimin [STM1669] [...]	158	5e-37
<input type="checkbox"/>	tr Q83T27	Invasin-like protein [t1573] [Salmonella typhi]	157	1e-36
<input type="checkbox"/>	tr Q8Z795	Invasin-like protein [STY1395] [Salmonella typhi]	156	1e-36
<input type="checkbox"/>	tr Q7WR47	Putative adhesin [BB0110] [Bordetella bronchiseptica (...]	85	5e-15
<input type="checkbox"/>	tr Q7W286	Putative adhesin [BPP0104] [Bordetella parapertussis]	85	6e-15
<input type="checkbox"/>	tr Q7WAX9	Putative outer membrane ligand binding protein [bipA] ...	70	1e-10
<input type="checkbox"/>	tr Q9APE8	Putative outer membrane ligand binding protein [bipA] ...	69	4e-10

<input type="checkbox"/>	tr	Q7VZ27	Putative outer membrane ligand binding protein [bipA] ...	69	4e-10
<input type="checkbox"/>	tr	Q7VR49	Putative adhesin [eaeH] [Candidatus Blochmannia florid...	67	1e-09
<input type="checkbox"/>	tr	Q52708	Outer membrane protein A (Fragment) [ompA] [Rickettsia...	53	3e-05
<input type="checkbox"/>	tr	Q6CD35	Similarity [YALI0C04136g] [Yarrowia lipolytica CLIB99]	53	3e-05
<input type="checkbox"/>	tr	Q82XT8	Hemolysin-type calcium-binding region:RTX N-terminal d...	51	1e-04
<input type="checkbox"/>	sp	Q52657	OMPA_RICCN Outer membrane protein A precursor (190 kDa...	50	2e-04
<input type="checkbox"/>	tr	Q6CPZ4	Kluyveromyces lactis strain NRRL Y-1140 chromosome E o...	50	2e-04
<input type="checkbox"/>	sp	Q8TFG9	YL61_SCHPO Hypothetical serine/threonine-rich protein ...	47	0.002
<input type="checkbox"/>	tr	Q9C105	SPAPB1E7.04c protein [SPAPB1E7.04c] [Schizosaccharomyc...	47	0.002
<input type="checkbox"/>	tr	Q722C9	Cell wall surface anchor family protein [LMOF2365_0805...	46	0.003
<input type="checkbox"/>	tr	Q76I98	Bacterial immunogloblin [is2-2] [Leptospira interrogan...	46	0.003
<input type="checkbox"/>	tr	Q7U7M8	Hypothetical [SYNW0953] [Synechococcus sp. (strain WH8...	45	0.004
<input type="checkbox"/>	tr	Q8FGD9	Hypothetical protein c2439 [c2439] [Escherichia coli O6]	45	0.006
<input type="checkbox"/>	tr	Q6KB38	Intimin zeta (Fragment) [eae] [Escherichia coli]	45	0.006
<input type="checkbox"/>	tr	Q6AHX5	Hypothetical protein DKFZp686O19206 [DKFZp686O19206] [...	45	0.006
<input type="checkbox"/>	sp	P15921	OMPA_RICRI Outer membrane protein A precursor (190 kDa...	45	0.007
<input type="checkbox"/>	tr	Q8VVW0	Intimin-lambda (Fragment) [eae-lambda] [Escherichia coli]	44	0.010
<input type="checkbox"/>	tr	Q8VLL9	Intimin (Fragment) [eae] [Escherichia coli]	44	0.010
<input type="checkbox"/>	tr	Q6KBV3	Intimin zeta (Fragment) (Fragment) [eae] [Escherichia ...	44	0.010

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sp      P19196      Invasin [Yersinia enterocolitica]      835 AA
      INVA YEREN                                     align

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Sbjct: 721 SKKFPSYATATYQFKPNLWVFSGTMSLQSSVEASRNCQRTDFTALIESARASNGSRSPDGT 780

Query: 781 LWGEWGSLATYDSA EWPSGNYWTKKTSTDFVTMDMTTGD IPTSAATAYPLCAEPQ 835
LWGEWGSLATYDSA EWPSGNYWTKKTSTDFVTMDMTTGD IPTSAATAYPLCAEPQ

Sbjct: 781 LWGEWGSLATYDSA EWPSGNYWTKKTSTDFVTMDMTTGD IPTSAATAYPLCAEPQ 835

tr Q56889 Invasin [invA] [Yersinia enterocolitica] 835 AA
align

Score = 1613 bits (4176), Expect = 0.0

Identities = 805/835 (96%), Positives = 811/835 (96%)

Query: 1 MYSFFNTLTVTKXXXXXXXXXXXXXXXXXXTYGFSQQHYFNSEALENPAEHNEAFNKIISTG 60
MYSFFNTLTVTK TYGFSQQ+YFNSEALENPAEHNEAFNKIISTG

Sbjct: 1 MYSFFNTLTVTKIIISRLILSIGLIFGIFTYGFSQQNYFNSEALENPAEHNEAFNKIISTG 60

Query: 61 TSLAVSGNASNITRSMVNDAAANQEVKHWLNRF GTTQVNVNFDKKFSLKESSLDWLLPWYD 120
TSLAVSGNASNITRSMVNDAAANQEVKHWLNRF GTTQVNVNFDKKFSLKESSLDWLLPWYD

Sbjct: 61 TSLAVSGNASNITRSMVNDAAANQEVKHWLNRF GTTQVNVNFDKKFSLKESSLDWLLPWYD 120

Query: 121 SASYVFFSQLGIRNKDSRNTLNIGAGVRTFQQSWMYGFNTSYDNDMTGHNHRIGVGAEAW 180
SASYVFFSQLGIRNKDSRNTLNIGAGVRTFQQSWMYGFNT YDNDMTGHNHRIGVGAEAW

Sbjct: 121 SASYVFFSQLGIRNKDSRNTLNIGAGVRTFQQSWMYGFNTFYDNDMTGHNHRIGVGAEAW 180

Query: 181 TDYLQLSANGYFRLNGWHQSRDFADYNERPASGGDIHV KAYLPALPQLGGKLYEQYRGE 240
TDYLQLSANGYFRLNGWHQSRDF DYNERPASGGDIHV KAYLPALPQLGGKLYEQYRGE

Sbjct: 181 TDYLQLSANGYFRLNGWHQSRDFVDYNERPASGGDIHV KAYLPALPQLGGKLYEQYRGE 240

Query: 241 RVALFGKDNLQSNPYAVTTGLIYTPIPFITLGV DQRMGKSRQHEIQWNLQMDYRLGESFR 300
RVALFGKDNLQSNPYAVTTGLIYTPIPFITLGV DQRMGKSRQHEIQWNLQMDYRLGESFR

Sbjct: 241 RVALFGKDNLQSNPYAVTTGLIYTPIPFITLGV DQRMGKSRQHEIQWNLQMDYRLGESFR 300

Query: 301 SQFSPAVVAGTRLLAESRYNLVERNPNIVLEYQKQNTIKLAFSPAVLSGLPGQVYSVSAQ 360
SQFSPAVVAGTRLLAESRYNLVERNPNIVLEYQKQNTIKLAFSPAVLSGLPGQVYSVSAQ

Sbjct: 301 SQFSPAVVAGTRLLAESRYNLVERNPNIVLEYQKQNTIKLAFSPAVLSGLPGQVYSVSAQ 360

Query: 361 IQSQSALQRILWNDAAQWVAAGGKLIPVSATDYNVVLPPYKMPAPASRTVGKTGESEAAVN 420
IQSQSALQRILW+DAQW+A GGKLIPVSAT+YNVVLPPYKMPAPASRTVGKTGESEAAVN

Sbjct: 361 IQSQSALQRILWDDAQWIAVGGKLIPVSATNYNVVLPPYKMPAPASRTVGKTGESEAAVN 420

Query: 421 TYTLSATAIDNHGSSNPATLTVIVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDS 480
TYTLSATAIDNHGSSNPATLTVIVQQPQFVITSEVTDDGALADGRTPITVKFTVTNID

Sbjct: 421 TYTLSATAIDNHGSSNPATLTVIVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDG 480

Query: 481 TPVAEQEGVITTSNGALPSKVTKKTD AQGVISIALTSFTVGVSVVTLDIQQQATVDVRF 540
TPVAEQEGVITTSNGALPSKVTKKTD AQGVISIALTSFTVG SVVTLDIQQQATVDVRF

Sbjct: 481 TPVAEQEGVITTSNGALPSKVTKKTD AQGVISIALTSFTVGGSVVTLDIQQQATVDVRF 540

Query: 541 AVLPPDVTNSSFNVSPSDIVADGSMQSILTFVPRNKNNFVSGITDLEFIQSGVPVTISP 600
AVLPPDVTNSSFNVSPSDIVADGSMQSILTFVPRNKNNFVSGITDLEFIQSGVPVTISP

Sbjct: 541 AVLPPDVTNSSFNVSPSDIVADGSMQSILTFVPRNKNNFVSGITDLEFIQSGVPVTISP 600

Query: 601 VTENADNYTASVVGNSVGVDITPQVGGESLDLLQKRITLYPVPKITGINVNGEQFATDK 660
VTENADNYTASVVGNSVGVDITPQVGGESLDLLQKRITLYP+PKIT I VNGEQFATDK

Sbjct: 601 VTENADNYTASVVGNSVGVDITPQVGGESLDLLQKRITLYPIPKITSIAVNGEQFATDK 660

Query: 661 GFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAASAPVDNQGKVNIAYKTYGSTVTVTAK 720
 GFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAASAPVDNQGKVNIAYKTYGSTVTVTAK
 Sbjct: 661 GFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAASAPVDNQGKVNIAYKTYGSTVTVTAK 720

Query: 721 SKKFPSYATATYQFKPNLWVFSGTMSLQSSVEASRNCQRTDFTALIESARASNGSRSPDGT 780
 SKKFPSYATATYQFKPNLWVFSGTMSLQSS+EASRNCQRTDFTALIESARASNGSRSPDGT
 Sbjct: 721 SKKFPSYATATYQFKPNLWVFSGTMSLQSSIEASRNCQRTDFTALIESARASNGSRSPDGT 780

Query: 781 LWGEWGLATYDSA EWPSGNYWTKKTSTDFVTMDMTTGDIPTSAATAYPLCAEPQ 835
 LWGEWGLATYDSA EWPSGNYWTKKTSTDFVTMDMTTG IPTSAATAYPLCAEPQ
 Sbjct: 781 LWGEWGLATYDSA EWPSGNYWTKKTSTDFVTMDMTTGAIPTSAATAYPLCAEPQ 835

sp P11922 **Invasin [Yersinia pseudotuberculosis]** 985 AA
 INVA_YERPS align

Score = 726 bits (1874), Expect = 0.0

Identities = 381/695 (54%), Positives = 481/695 (68%), Gaps = 43/695 (6%)

Query: 45 NPAEHNEAFNKIISTGTSLAVSGNASNITRSMVNDAAANQEVKHWLNRFGTQVNVNFDKK 104
 N + EA NK+ISTG LA SG AS++ SMV DA NQE+K WLNRFGT QVN+NFDK
 Sbjct: 102 NKEQETEAVNKMISTGARLAASGRASDVASHMVGDVAVNQEIQLWLNRFGTQVNLNFDKN 161

Query: 105 FSLKESSLDWLLPWYDSASVFFSOLGIRNKDSRNTLNIGAGVRTFQQSWMYGFNTSYDN 164
 FSLKESSLDWL PWYDSAS++FFSOLGIRNKDSRNTLN+G G+RT + W+YG NT YDN
 Sbjct: 162 FSLKESSLDWLAPWYDSASFLFFSOLGIRNKDSRNTLNLGVGIRTLENGWLYGLNTFYDN 221

Query: 165 DMTGHNHRIGVGAEAWTDYQLQSANGYFRLNGWHQSRDFADYNERPASGGDIHV KAYLPA 224
 D+TGHNHRIG+GAEAWTDYQL+ANGYFRLNGWH SRDF+DY ERPA+GGD+ AYLPA
 Sbjct: 222 DLTGHNHRIGLGAEAWTDYQLAANGYFRLNGWHSSRDFSDYKERPATGGDLRANAYLPA 281

Query: 225 LPQLGGKLYEQYRGERVALFGKDNLQSNPYAVTTGLIYTPIPFITLGVDQRMGKSRQHE 284
 LPQLGGKL YEQY GERVALFGKDNLQ NPYAVT G+ YTP+P +T+GVDQRMGKS +HE
 Sbjct: 282 LPQLGGKLMYEQYTGGERVALFGKDNLQRNPYAVTAGINYPVPLLTGVDQRMGKSSKHE 341

Query: 285 IQWNLQMDYRLGESFRSQFSPAVVAGTRLLAESRYNLVERNPNIVLEYQKQNTIKLAFSP 344
 QWNLQM+YRLGESF+SQ SP+ VAGTRLLAESRYNLV+RN NIVLEYQKQ +KL SP
 Sbjct: 342 TQWNLQMNRYRLGESFQSQLSPSAVAGTRLLAESRYNLVDRNNNIVLEYQKQVVKLTLSLSP 401

Query: 345 AVLSGLPGQVYSVSAQIQSQSALQRI LWND AQWVAAGGKLIPVSATDYNVLPYPKMAP 404
 A +SGLPGQVY V+AQ+Q SA++ I+W+DA+ +AAGG L P+S T +N+VLPPYK A
 Sbjct: 402 ATISGLPGQVYQVNAQVQGASAVREIVWSDAELIAAGGTLTPLSTTQFNLVLPYPKRTAQ 461

Query: 405 ASRTVGKTGESEAAVNTYTL SATAIDNHGNSNPATLTVIVQQPQFVITSEVTDDGALAD 464
 SR + N Y+LSA A+D+ GN SN TL+V VQQPQ +T+ V DGA A+
 Sbjct: 462 VSRVT-----DDL TANFYLSALAVDHQGNRSNSFTLSVTVQQPQLTLTAAVIGDGAPAN 516

Query: 465 GRTPITVKFTVTNIDSTPVAEQEGVITTSNGALPSKVTKKTD AQGVISIALTSFTVGVS 524
 G+T ITV+FTV + + P+A QE VITT+NGALP+K+T+KTDA GV IALT+ T GV+V
 Sbjct: 517 GKTAITVEFTVADFEKGPLAQEVVITTNNGALPNKITEKTDANGVARIALTNTTGDGVT 576

Query: 525 VTLDIQGQQATVDVRFVAVLPPDVTNSSFNVSPSDIVADGSMQSILTFVPRKNKNEFVSGI 584
 VT +++GQ+ +VD F S+ P+ I+ADG M S +T ++ + +G
 Sbjct: 577 VTAEVEGQRQSVDFHVKGTIAADKSTLAAVPTSIIADGLMASTITLELKDTYGDQPAGA 636

Query: 585 T---DLEFIQSGVPVTISPVTENAD-NYASVVGNSVGVDITPQVGGESLDLLQKRITL 640
 D GV +T++ D Y+A + +G +T +V G +
 Sbjct: 637 NVAFDTTLGNMGV-----ITDHNDGTYSAPLTSTTLGVATVTVKVDGAA----- 680

Query: 641 YPVPKITGINVNGEQFATDKGFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAASAPVDN 700
 + VP +T VN F D P +++F + D +A+ T SS + PVD
 Sbjct: 681 FSVPSVT---VN---FTAD---PIPDAGRSSFTVSTPDILADGTM-----SSTLSFVPVVDK 727

Query: 701 QGKV-----NIAYKTYGSTVTVTAKSKKFPSYTAT 730
 G +++ G V+++ +++ SYTAT
 Sbjct: 728 NGHFIQSGMQLSFTQNGVVPVSISPITEQPDSYTAT 762

Score = 386 bits (991), Expect = e-105

Identities = 205/376 (54%), Positives = 262/376 (69%), Gaps = 10/376 (2%)

Query: 462 LADGRTPITVKFTVTNIDSTPVAEQEGVITTSNGALPSKVTKKTDACQGVISIALTSFTVG 521
 +ADG T+ + + P A T+ G + +T D G S LTS T+G
 Sbjct: 612 IADGLMASTITLELKDTYGDQPAGANVAFDITLGNM-GVITDHND--GTYSAPLTSTTLG 668

Query: 522 VSVVTLDIQGGQ---ATVDVRFVFLP-PDVTNSSFNVSFSDIVADGSMQSILTFVPRNKN 577
 V+ VT+ + G +V V F P PD SSF VS DI+ADG+M S L+FVP +KN
 Sbjct: 669 VATVTVKVDGAASFVPSVTVNFTADPIPDAGRSSFTVSTPDILADGTMSSTLSFVPVDKN 728

Query: 578 NEFVSGITDLEFIQSGVPVTISPVTENADNYASVVGNSVGVDITPQVGGESLDLLQKR 637
 F+SG+ L F Q+GVPV+ISP+TE D+YTA+VVGNSVGDV ITPQV L LQK+
 Sbjct: 729 GHFISGMQLSFTQNGVVPVSISPITEQPDSYTATVVGNSVGVDITPQVDTLILSTLQKK 788

Query: 638 ITLYPVPKITGINVNGEQFATDKGFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAASAP 697
 I+L+PVP +TGI VNG+ FATDKGFPKT F ATFQL M++DVANNTQY+W+SS+ +
 Sbjct: 789 ISLFPVPTLTGILVNGQNFATDKGFPKTIFKNATFQLQMDNDVANNTQYEWSSSFTPNVS 848

Query: 698 VDNQGVNIAYKTYGSTVTVTAKSKKFPSYTATYQFKPNLWVFSGTMSLQSSVEASRNCQ 757
 V++QG+V I Y+TY S V VTAKSKKFPSY+ +Y+F PN W++ G SL SS+EASR CQ
 Sbjct: 849 VNDQGQVTITYQTY-SEVAVTAKSKKFPSYSVSRYFYPNRWIYDGGRLVSSLEASRQCQ 907

Query: 758 RTDFTALIESARASNGSRSPDGTLLWGEWGSLATYDSAEPWPSGNYWTKKTSTDFVTMDMTT 817
 +D +A++ES+RA+NG+R+PDGTLLWGEWGSL Y S++W SG YW KKTSTDF TM+M T
 Sbjct: 908 GSDMSAVLESSRATNGTRAPDGTLLWGEWGSLTAY-SSDWQSGEYVWKKTSTDFETMNMDT 966

Query: 818 GDI-PTSAATAYPLCA 832
 G + P A A+PLCA
 Sbjct: 967 GALQPGPAYLAFPLCA 982

tr Q56937 Invasin [inv] [Yersinia pestis] 987 AA
 align

Score = 721 bits (1861), Expect = 0.0

Identities = 381/696 (54%), Positives = 480/696 (68%), Gaps = 44/696 (6%)

Query: 45 NPAEHNEAFNKIISTGTSLAVSGNASNITRSMVNDAAEQEVKHWLNRFGTTQVNVNFDKK 104
 N + EA NK+ISTG LA SG AS++ SMV DA NQE+K WLNRFGT QVN+NFDK
 Sbjct: 103 NKEQETEAVNKMISTGARLAASGRASDVASHMVGDAVNQEIKQWLNRFGTQVNLNFDKN 162

Query: 105 FSLKESSLDWLLPWYDSASYVFFSQLGIRNKDSRNTLNIGAGVRTFQQSWMYGFNTSYDN 164

FSLKESSLDWL PWYDSAS++FFSQLGIRNKDSRNTLN+G G+RT + W+YG NT YDN
 Sbjct: 163 FSLKESSLDWLAPWYDSASFLFFSQLGIRNKDSRNTLN+G G+RT + W+YG NT YDN 222
 Query: 165 DMTGHNHRIGVGAEAWTDYLQLSANGYFRLNGWHQSRDFADYNERPASGGDIHVKAYLPA 224
 D+TGHNHRIG+GAEAWTDYLQL+ANGYFRLNGWH SRDF+DY ERPA+GGD+ AYLPA
 Sbjct: 223 DLTGHNHRIGLGAEAWTDYLQLAANGYFRLNGWHSSRDFSDYKERPATGGDLRANAYLPA 282
 Query: 225 LPQLGGKLYEQYGERVA-LFGKDNLQSNPYAVTTGLIYTPIPFITLQVDQRMGKSRQH 283
 LPQLGGKL YEQY GERV LFGKDNLQ NPYAVT G+ YTP+P +T+GVDQRMGKS +H
 Sbjct: 283 LPQLGGKLMYEQYTGERVALLFGKDNLQRPYAVTAGINYPVPLLTGVDQRMGKSSKH 342
 Query: 284 EIQWNLMQMDYRLGESFRSQSPAVVAGTRLLAESRYNLVERNPNIVLEYQKQNTIKLAFA 343
 E QWNLMQ+YRLGESF+SQ SP+ VAGTRLLAESRYNLV+RN NIVLEYQKQ +KL S
 Sbjct: 343 ETQWNLMQNYRLGESFQSQLSPSAVAGTRLLAESRYNLVDRNNIVLEYQKQVVKLTLS 402
 Query: 344 PAVLSGLPGQVYSVSAQIQSQSALQIRILWDAQWVAAGGKLIPVSATDYNVVLPPYKPA 403
 PA +SGLPGQVY V+AQ+Q SA++ I+W+DA+ +AAGG L P+S T +N+VLPPYK A
 Sbjct: 403 PATISGLPGQVYQVNAQVQASAVREIVWSDAELIAAGGTLTPLSTTQFNLVLPPYKRTA 462
 Query: 404 PASRTVGKTGESEAAVNTYTLATAIDNHGNSNPATLTVIVQQPQFVITSEVTDDGALA 463
 SR + N Y+LSA A+D+ GN SN TL+V VQQPQ +T+ V DGA A
 Sbjct: 463 QVSRVT-----DDLTA NFYSLSALAVDHQGNRSNSFTLSVTVQQPQLTLTAAVIGDGAPA 517
 Query: 464 DGRTPIITVKFTVTNIDSTPVAEQEGVITTSNGALPSKVTKKTDAGQVISIALTSFTVGVS 523
 G+T ITV+FTV + + P+A QE VITT+NGALP+K+T+KTDA GV IALT+ T GV+
 Sbjct: 518 SGKTAITVEFTVADFEGKPLAGQEVVITTNNGALPNKITEKTDANGVARIALTNTTDTGVT 577
 Query: 524 VVTLDIQGQQATVDVRFVAVLPDVTNSSFVSPSDIVADGSMQSILTFVPRNKNNEFVSG 583
 VVT +++GQ+ +VD F S+ P+ I+ADG M S +T ++ + +G
 Sbjct: 578 VVTAEEVGQRQSVDTDFVKGITIAADKSTLAAVPTSIIADGLMASTITLELKDTYGDPQAG 637
 Query: 584 IT---DLEFIQSGVPVTISPVTENAD-NYASVVGNSVGDVDITPQVGESLDLLQKRIT 639
 D GV +T++ D Y+A + ++G +T +V G +
 Sbjct: 638 ANVAFDITLGNMGV-----ITDHNDGTYSAPLTSTTLGVATVTVKVDGAA----- 682
 Query: 640 LYPVPKITGINVNGEQFATDKGFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAASAPVD 699
 + VP +T VN F D P +++F + D +A+ T SS + PVD
 Sbjct: 683 -FSVPSVT---VN---FTAD---PIPDAGRSSFTVSTPDILADGTM---SSTLSFVPVD 728
 Query: 700 NQGVK----NIAYKTYGSTVTVTAKSKKFPSYTAT 730
 G +++ G V+++ +++ SYTAT
 Sbjct: 729 KNGHFISGMQGLSFTQNGVPPVSPITEQPDSYTAT 764

Score = 380 bits (975), Expect = e-104

Identities = 201/376 (53%), Positives = 260/376 (68%), Gaps = 10/376 (2%)

Query: 462 LADGRTPIITVKFTVTNIDSTPVAEQEGVITTSNGALPSKVTKKTDAGQVISIALTSFTVG 521
 +ADG T+ + + P A T+ G + +T D G S LTS T+G
 Sbjct: 614 IADGLMASTITLELKDTYGDPQAGANVAFDITLGNM-GVITDHND--GTYSAPLTSTTLG 670
 Query: 522 VSVVTLDIQGQQ--ATVDVRFVAVLP-PDVTNSSFVSPSDIVADGSMQSILTFVPRNKN 577
 V+ VT+ + G +V V F P PD SSF VS DI+ADG+M S L+FVP +KN
 Sbjct: 671 VATVTVKVDGAASFVPSVTVNFTADPIPDAGRSSFTVSTPDILADGTMSSTLSFVPVDKN 730
 Query: 578 NEFVSGITDLEFIQSGVPVTISPVTENADNYASVVGNSVGDVDITPQVGESLDLLQKR 637
 F+SG+ L F Q+GVPV+ISP+TE D+YTA+VVG+N+ GDV ITP V L LQK+
 Sbjct: 731 GHFISGMQGLSFTQNGVPPVSPITEQPDSYTATVVGNTAGDVTITPLVDTLILSTLQKK 790

Query: 638 ITLYPVPKITGINVNGEQFATDKGFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAASAP 697
I+L+PVP +TGI VNG+ FATDKGFPKT F ATFQL M++DVANNTQY+W+SS+ +
Sbjct: 791 ISLFPVPTLTGILVNGQNFATDKGFPKTIFKNATFQLQMDNDVANNTQYEWSSSFTPNVS 850

Query: 698 VDNQGKVNIAKYTGSTVTVTAKSKKFPSYATYQFKPNLWVFSGTMSLQSSVEASRNCQ 757
V++QG+V I Y+TY S V VTAKSKKFPSY+ +Y+F PN W++ G SL SS+EASR CQ
Sbjct: 851 VNDQGQVTITYQTY-SEVAVTAKSKKFPSYSVSYRFYPNRWIYDGGTSLVSSIEASRQCQ 909

Query: 758 RTDFTALIESARASNGSRSPDGTWGEWGSLATYDSAEWPSGNYWTKKTSTDFVTMDMTT 817
+D +A++ES+RA+NG+R+PDGTWGEWGS L Y S++W SG YW K+TSTDF TM+M T
Sbjct: 910 GSDMSAVLESSRATNGTRAPDGTWGEWGS LTAY-SSDWQSGEYWVKRTSTDFETNMNMT 968

Query: 818 GDI-PTSAATAYPLCA 832
G + P A A+PLCA
Sbjct: 969 GLLQPGPAYLAFFPLCA 984

tr Q8ZA73 Putative invasin (Hypothetical) [YPO3944] [Yersinia pestis] 3013 AA

align

Score = 428 bits (1100), Expect = e-118
Identities = 265/703 (37%), Positives = 382/703 (53%), Gaps = 38/703 (5%)

Query: 66 SGNASNITRSMVNDAAANQEVKHWLNRFGTQVNVNFDKKFSLKESSLDWLLPWYDSASYV 125
S ASN+ RS V + N + WLN+FGT +V +N D F L S+LD L+P DS S +
Sbjct: 178 SDAASNMARSAVTNEINASSQQWLNQFGTARVQLNVDSDFKLDNSALDLLVPLKDSSESL 237

Query: 126 FFSQLGIRNKDSRNTLNIGAGVRTFQQSWMYGFNTSYDNDMTGHNHRIGVGAEAWTDYLQ 185
F+QLG+RNKDSRNT+NIGAG+R +Q WMYG NT +DND+TG N R+GVGAE TDYL+
Sbjct: 238 LFTQLGVRNKDSRNTVNIGAGIRQYQGDWYGANTFFDNDLTGKNRRVGVGAEVATDYLK 297

Query: 186 LSANGYFRLNGWHQSRDFADYNERPASGGDIHV KAYLPALPQLGGKLYEQYRGERVALF 245
SAN YF L GWHQSRDF+ Y+ERPA G DI +AYLPA PQLGGKL YE+YRG+ VALF
Sbjct: 298 FSANTYFGLTGWHQSRDFSSYDERPADGFDIRTEAYLPAYPQLGGKLYEYRGDEVALF 357

Query: 246 GKDNLQSNPYAVTTGLIYTPIPFITLGVDQRMGKSRQHEIQWNLQMDYRLGESFRSQFSP 305
GKD+ Q +P+AVT G+ YTP+P +T+G + R GK + N+Q++YR+G+ + Q
Sbjct: 358 GKDDRQKDPHAVTLGVNYTPVPLVTIGAEHREGKGNNTSVNVQLNYRMGQPWNDQIDQ 417

Query: 306 AVVAGTRLLAESRYNLVERNPNIVLEYQKQNTIKLAFSPAVLSGLPGQVYSVSAQIQSQS 365
+ VA R LA SRY+LVERN NIVL+Y+KQ I L P +SG G +++AQ++++
Sbjct: 418 SAVAANRTLAGSRYDLVERN NIVLDYKKQELIHLVL-PDRISGSGGGAITLTAQVRAKY 476

Query: 366 ALQRIWLNDAQWVAAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTGESEAAVNTYTLS 425
RI W+ AGG P++ + +V LP Y+ + S NT+T+S
Sbjct: 477 GFSRIEWDATPLENAGGSTSPLTQSSLSVTLPPFYQHILRTS-----NTHTIS 523

Query: 426 ATAIDNHGSSNPATLTIVIQQPQFVITSEV--TDDGALADGRTPITVKFTVTNIDSTPV 483
A A D GN+SN A ++ V +P+ ++ S + T D A A+G TV+ TVT+ D P+
Sbjct: 524 AVAYDAQGNASNRAVTSIEVTRPETMVISHLATTIDNATANGIATNTVQATVTDGDGQPI 583

Query: 484 AEQEGVITTSNGALPSKVTKKTDAGGVISIALTSFTVGVSVVTLDIQQQATVDVRFVAV- 542
Q + A S +T A G S LT GVS V++ + +VD F
Sbjct: 584 IGQLINFAVNTQATLSTTEARTGANGTASTTLTHTVSGVSRVSVTLGSSSRSDTTTFVAD 643

Query: 543 -LPPDVTNSSFVNSPSDIVADGSMQSILTFVPRNKNNEFVSGITDLEFIQSGVPVTISP 601
 ++T ++ V+ +D VA+GS +++ + V+ + + +G V V
 Sbjct: 644 ESTAEITAANLTVTNDSDVANGSDTNVVRKVTDAYTNAVANQSVIFSASNGATVIDQTV 703

Query: 602 TENADNYTASVVGNSVGDVD-ITPQVGESLDLLQKRITLYPVPKITGINVNGEQFATDK 660
 NA+ S + N+ V +T +GG+S Q T P V A
 Sbjct: 704 ITNAEGIA DSTLTNTTAGVSVVTATLGGQS---QQVD TTFKPGSTAAISLVKLADRAVAD 760

Query: 661 GFPKTTFNKATFQLVMNDDVAN-----NTQYDWTSSYAASAP-VDNQGKVNIAY---K 709
 G ++ Q+V+ D N + Q D + AS P G +N + +
 Sbjct: 761 G-----IDQNEIQVVL RDGTGNAV PNPVMSIQADNGAIVVASTPNTGVDGTINATFTNLR 815

Query: 710 TYGSTVTVTAKSKKFPSYTATYQFKPNLWVFSGTMSLQSSVEA 752
 S V+VT+ + + T T+ P V S ++ ++ +A
 Sbjct: 816 AGESVSVSTSPALVGMTMTMTFSADPRTAVVSTLAAIDNNAK 858

Score = 122 bits (305), Expect = 4e-26

Identities = 123/477 (25%), Positives = 199/477 (40%), Gaps = 28/477 (5%)

Query: 374 DAQWVAAGGKLIPVSATDYNVVLPPYKMPAPASRTVGKTGESEAAVNTYTLSATAIDNHG 433
 DA GG+ + SAT+ + ++ +V + S A + ++ T + N+
 Sbjct: 2548 DANQNPVGGQQVAFSATNEVTLTESNGSISTPEGSVLLSVTSTQA-GVHPITGLTVSNY 2606

Query: 434 NSSNPATLTVIVQQPQFVITSEVTDGALADGRTPITVKFTVTNIDSTPVAEQEGVITTS 493
 + A Q + T V D+ ALADG T V+ V + VA+ T +
 Sbjct: 2607 TDTFGAAFIANKNTAQ-LSTLMVVDNNALADGVTRNQVRAHVVDSTGNSVADMAVTF TAN 2665

Query: 494 NGALPSKVTKKTDAAQGVISIALTSFTVGVSVVT--LDIQGQQATVDVRFVLPDVTNSS 551
 GA SKVT TD G LT+ VGV+VVT L G TVD F P + +
 Sbjct: 2666 RGAQLSKVTVLTDNNGDAVNLTLSLVGVTVVTA KLGTAGTPLTVDTVFTAGP--LATLT 2723

Query: 552 FNVSPSDIVADGSMQSILTFVPRNKNNEFVSGITDLEFIQSGVPVTISP-VTENADNYTA 610
 + ++ AD S + + ++ + + G +G +T + NA+
 Sbjct: 2724 LVTTVNNAFADNSATNTVQATLKDVS GNPIVGEVVAFAASNGATITATDGGVSNANGIVL 2783

Query: 611 SVVGNSVG DVDITPQVGESLDLLQKRITLYPVPKITGINVNGEQFATDKGFPKTTFNKA 670
 + + N V V L + T + K + VNG F D GFP T F A
 Sbjct: 2784 ATLTNGTAGVS---TVTAT IETLTETDTTFIAMKNLDVTVNGTTFNGDAGFPTTG FVGA 2840

Query: 671 TFQLVMNDDVANNTQYDWTSSYAASAPVDNQKV--NIAYKTYGSTVTVTAKSKKFPSYT 728
 TF++ D N+ YDW+SS A V G V N + T T+T++A K S
 Sbjct: 2841 TFKVNSGGD---NSLYDWSSSAPALVSVSGDGVVTFNAVFP TGTPTITISATPKGGGS-P 2896

Query: 729 ATYQFKPNLWVFSGTMSLQSSVEASRNCQRTDF-----TALIESARASNGSRSPDGLWG 783
 +Y F+ N W + + + +A +C+ + T + +A +G R+ G LW
 Sbjct: 2897 LSY SFRVNQWFINNNGATLNRADAITHCENVGYTMTPTSTQVTNAATWMSGKRAV-GNLWS 2955

Query: 784 EWGSLATYDSA EW-PSGNYWTKKT--STDFVTMDMTTGDIPTSA--ATAYPLCAEP 834
 EWG + Y + W P+ +W ++ + + ++TG + T A + +C P
 Sbjct: 2956 EWGDFSAYTAPGWVPAEFFWLSNNHDASTALAI GLSTGTLT T MGDFMAITHVMCTRP 3012

Score = 60.1 bits (144), Expect = 2e-07

Identities = 54/203 (26%), Positives = 86/203 (41%), Gaps = 7/203 (3%)

Query: 418 AVNTYTLSATAIDNH--GNSSNPATLTVIVQQPQFVITSE--VTDDGALADGRTPITVK 472

A T+TL+ T++ GN T I + I + +T + ALADG +
 Sbjct: 1983 ATLTHTLAGTSVVTARVGNRVQSKDITFIADRTTATIRASDLTITRNNALADGVATNAAR 2042
 Query: 473 FTVTNIDSTPVAEQEGVITTSNGALPSKVTKKTDAGQVISIALTSFTVGVSVVTLDI--Q 530
 VT+ + PV T+ NGAL + + TD+ G S T T G+S VT I
 Sbjct: 2043 VIVTDANGNPVPSMFVGYTSDNGALLTPTSGMTDSSGTFSTTFTHTTAGISKVTAIVTM 2102
 Query: 531 GQQATVDVRFVAVLPPDVTNSSFNVSPSDIVADGSMQSILTFVPRNKNEFVSGITDLEFI 590
 G T D F S V +D +A+ S ++I+ ++ + V+G+
 Sbjct: 2103 GISQTKDAVFIADRSTAHVSELIVVKNDLANNSDRNIVQAHIKDAHGNVVTGMNVNFS 2162
 Query: 591 QSGVPVTISPVTENADNYTASVV 613
 V +T + VT N+ Y + +
 Sbjct: 2163 TENVTLTANTVTTNSQGYAENTL 2185

Score = 53.5 bits (127), Expect = 2e-05

Identities = 62/250 (24%), Positives = 93/250 (36%), Gaps = 10/250 (4%)

Query: 373 NDAQVWAAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTGESEAAVNTYTLSATAIDNH 432
 N Q V + PV T VV A + +G TG A T T + N
 Sbjct: 962 NSVQAVVSDSGGNPV--TGATVVFSSSTNATAQVTTVIGTTGVDGIATATLTNTVAGTSNV 1019
 Query: 433 G---NSSNPATLTIVVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDSTPVAEQEGV 489
 ++ N T V IT +GA+ADG V V + + P+ V
 Sbjct: 1020 VATIDTVNANIDTAFVAGAVATITLTAPVNGAVADGADTNQVDALVEDANGNPITGAADV 1079
 Query: 490 ITTSNGALPSKVTKKTDAGQVISIALTSFTVGVSVVTLDIQGGQATVDVRFVAVLPPDVTN 549
 +++NGA T T GV S LT G S V + A +D F + V
 Sbjct: 1080 FSSANGATILSSTMTGTVNGVASTLLTHTVAGTSNVVATVDTVNANIDTTF--VAGAVAT 1137
 Query: 550 SSFNVSPSDIVADGSMQSILTFVPRNKNEFVSGITDLEFIQSGVPVTISPVT--TENADN 607
 + + VADG+ + + V + + V+G + F + I+ V T AD
 Sbjct: 1138 ITLTPVNGAVADGANSNSVQAVVSDSDGNPVTGAA-VVFSSANATAQITTVIGTTGADG 1196
 Query: 608 YTASVVGNSV 617
 + + N+V
 Sbjct: 1197 IATATLTNTV 1206

Score = 51.6 bits (122), Expect = 6e-05

Identities = 63/269 (23%), Positives = 108/269 (39%), Gaps = 30/269 (11%)

Query: 458 DDGALADGRTPITVKFTVTNIDSTPVAEQEGVITTSNGALPSKVTKKTDAGQVISIALTS 517
 +DGA+ADG V+ V ++ V V + NG + +TDA G + +++
 Sbjct: 2226 NDGAVADGIQTNRVEARVYDVSDNLVPNSNVVFSADNGGQLVQNDVQTDALGSAYVTVS 2285
 Query: 518 FTVGVSVVTLDIQGGQATVDVRFVAVLPPDVT--NSSFNVSPSDIVADGSMQSILTFVPRN 575
 GV+ VT+ G A+ F T F ++ + VA+G +++ + +
 Sbjct: 2286 INTGVTKVTVTADGVSASTTTTTFIADRTATLVTRFLITHDNAVANGVVENRVLHLVD 2345
 Query: 576 KNEFVSGITDLEFIQSGVPVTISPVTENADNYTASVVGNSV-GDVDITPQVGESLDLL 634
 N+ VSG+ +G + S +T+ + + V+ N++ G D+T
 Sbjct: 2346 ANDNSVSGVEVNFSAITNGASINASAITD-INGFAIGVLTNTLSGSPSDVT----- 2393
 Query: 635 QKRITLYPVPKITGINVNGEQFATDKGFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAA 694
 +TL + V QF D T N AT V+ DD A D ++
 Sbjct: 2394 ---VTLVTPGGTESLTVT-PQFIAD---INTANIATGDFVIIDDGAVANSVD--ANEVR 2443

Query: 695 SAPVDNQGKVNIAYKTY-----GSTVTVT 718
+ DNQG Y G+T+T +
Sbjct: 2444 ARVTDNQGNIAIGYSVVFSSQNGATITTS 2472

Score = 48.5 bits (114), Expect = 5e-04
Identities = 72/292 (24%), Positives = 101/292 (33%), Gaps = 39/292 (13%)

Query: 373 NDAQWVAAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTGESEAAVNTYTLSATAIDNH 432
N Q V + PV T VV A + +G TG A T T + N
Sbjct: 1155 NSVQAVVSDSDGNPV--TGAAVVFSSANATAQITTVIGTTGADGIATATLTNTVAGTSNV 1212

Query: 433 G---NSSNPATLTVIVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDSTPVAEQEGV 489
++ N T V IT +GA+ADG V V + + + V
Sbjct: 1213 VATIDTVNANIDTAFVAGAVATITLTAPVNGAVADGADTNQVDALVQDANGNAITGAADV 1272

Query: 490 ITTSNGALPSKVTKKTDAGQVISIALTSFTVGVSVVTLDIQGGQATVDVRFVLPDPVTN 549
+++NGA T T GV S LT G S V I A +D F + V
Sbjct: 1273 FSSANGADIIAPTMTGTVNGVASTLLTHTVAGTSNVVATIDTISANIDTAF--VAGAVAT 1330

Query: 550 SSFNVSPSDIVADGSMQSILTFVPRKNNEFVSG----- 583
+ + VADG+ + + + N ++G
Sbjct: 1331 ITLTAPVNGAVADGADTNQVDALVEDANGNPITGAAVVFSSANGATILSSTMNTGVNGVA 1390

Query: 584 ---ITDLEFIQSGVPVTISPVTENADNYTASVVGNSVGDVDITPQVGESLD 632
+T S V TI VTEN D TA V G +V + +T V G D
Sbjct: 1391 STFLTHTVAGTSNVVATIGSVTENID--TAFVAG-AVATITLTAPVNGAVAD 1439

Score = 47.0 bits (110), Expect = 0.001
Identities = 46/178 (25%), Positives = 69/178 (37%), Gaps = 5/178 (2%)

Query: 442 TVIVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDSTPVAEQEGVITTSNGALPSKV 501
T V IT +GA+ADG V V + + P+ V +++NGA
Sbjct: 1321 TAFVAGAVATITLTAPVNGAVADGADTNQVDALVEDANGNPITGAAVVFSSANGATILSS 1380

Query: 502 TKKTDAGQVISIALTSFTVGVSVVTLDIQGGQATVDVRFVLPDPVTNSSFNVSPSDIVA 561
T T GV S LT G S V I +D F + V + + VA
Sbjct: 1381 TMNTGVNGVASTFLTHTVAGTSNVVATIGSVTENIDTAF--VAGAVATITLTAPVNGAVA 1438

Query: 562 DGSMQSILTFVPRKNNEFVSGITDLEFIQSGVPVTISPV--TENADNYTASVVGNSV 617
DG + + V + + V+G T + F + I+ V T AD + + N+V
Sbjct: 1439 DGVNTNSVQAVVSDSDGNAVGTAT-VVFSSANATAQITTVIGTTGADGIATATLTNTV 1495

Score = 45.1 bits (105), Expect = 0.006
Identities = 52/210 (24%), Positives = 90/210 (42%), Gaps = 15/210 (7%)

Query: 425 SATAIDNHGSSNPATLTVI--VQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDSTP 482
S T I G A +T + V Q +TS + D LA+G+ + VT+
Sbjct: 1595 SNTVIAISGAHQGYARVTFVADVSTAQLKLTSLF--DNQLANGKAGNIAQALVTD AHDNL 1652

Query: 483 VAEQEGVITTSNGALPSKVTKKTDAGQVISIALTSFTVGVSVV--TLDIQGGQATVDVRF 540
+A Q NGA+ + A G++ + + G++ V TLD GQ T++ F
Sbjct: 1653 LANQSVSFALDNGAVIESQGDASSAGIVLMRFNNTLAGMTTVTATLDSTGQTETLETHF 1712

Query: 541 A---VLPPDVTNSSFNVSPSDIVADGSMQSILTFVPRKNNEFVSGITDLEFIQSGVPVT 597

++T + N ++I + +Q ++T V N N V +T SG+ +T
 Sbjct: 1713 VAGKAASIEMTMTKDNAVANNIDTN-EVQVLVTDVDGNAINGAVVNLTS---NSGMNIT 1767

Query: 598 ISPV TENAD-NYTASVVGNSVGDVDITPQV 626

+ VT +D TA++ G + I ++

Sbjct: 1768 PNSVTTGSDGTATATLHTLAGSLPINARI 1797

Score = 43.9 bits (102), Expect = 0.013

Identities = 34/114 (29%), Positives = 51/114 (43%), Gaps = 4/114 (3%)

Query: 456 VTDDGALADGRTPITVKFTVTNIDSTPVAEQEGVITTSNGALPSKVTKKTDAGGVISIAL 515

+ DDGA+A+ V+ VT+ +A V ++ NGA + + T G S L

Sbjct: 2427 IIDDGAVANSVDANEVRARVTDNQGNIAIGYSVVFSSQNGATIT-TSGITGVDGWASAKL 2485

Query: 516 TSFTVGVS VVTLDIQGGQATVDVRFVLPDVTNSS---FNVSPSDIVADGSMQ 566

T G S + + ATV DV+ ++ FN +P I+ADG MQ

Sbjct: 2486 THIKAGESGILARLSRPMATVHTLMPYFIADVSTATLQLFNFNPIPIIADGVMQ 2539

Score = 43.9 bits (102), Expect = 0.013

Identities = 59/303 (19%), Positives = 120/303 (39%), Gaps = 28/303 (9%)

Query: 424 LSATAIDNHGSSNPATLTVIVQQPQFVITSE--VTDDGALADGRTPITVKFTVTNIDST 481

++AT + + G+S N T + + S+ V D A+AD V VT+

Sbjct: 1893 VTATVSS-GSSRNIDTTFIADVTTAHIAASDLMVIVDDAVADNLDKNEVHARVTDAGN 1951

Query: 482 PVAEQEGVITTSNGALPSKVTKKTDAGGVISIALTSFTVGVS VVTLDIQGGQATVDVRF 541

++ Q + T+ NGA + V +D G+ LT G SVVT + + + D F

Sbjct: 1952 VLSGQTVIFTSNGAAITTVNGISDGDGLTKATLHTLAGTSVVTARVGNRVQSKDTTFI 2011

Query: 542 V--LPPDVTNSSFNVSPSDIVADGSMQSILTFVPRNKNNEFVSGITDLEFIQSGVPVT-I 598

+ S ++ ++ +ADG + + + N V + +G +T

Sbjct: 2012 ADRTTATIRASDLTITRNALADGVATNAARVIVTDANGNPVPSMFVGYTSDNGALLTPT 2071

Query: 599 SPVTENADNYTASVVGNSVGDVDITPQVGESLDLLQKRITLYPVPKITGINVNGEQFAT 658

S +T+++ ++ + + G +T + + + + F

Sbjct: 2072 SGM TDSSGTFSTTFHTTAGISKVTAAIVTMGISQTKDAV-----FIA 2114

Query: 659 DKGFPKTTFNKATFQLVMNDDVANNTQYDWTSSYAASAPVDNQGVNIAYKTYGSTVTVT 718

D ++T + + +V ND +ANN+ + ++ A + +N+ + VT+T

Sbjct: 2115 D----RSTAHVSELIVVKNDSLANNSDRNIVQAHIKDAHGNVVTGMNVNFSA-TENVTLT 2169

Query: 719 AKS 721

A +

Sbjct: 2170 ANT 2172

Score = 39.3 bits (90), Expect = 0.31

Identities = 34/158 (21%), Positives = 64/158 (39%), Gaps = 1/158 (0%)

Query: 459 DGALADGRTPITVKFTVTNIDSTPVAEQEGVITTSNGALPSKVTKKTDAGGVISIALTSF 518

D A+ADG ++ + + V I NGA+ T T G I+ T+

Sbjct: 755 DRAVADGIDQNEIQVVL RDGTGNAV PNPVMSIQADNGAIVVASTPNTGVDGTINATFTNL 814

Query: 519 TVGVSVVTLDIQGGQA-TVDVRFVLPDVTNSSFNVSPSDIVADGSMQSILTFVPRNKN 577

G SVV++ T+ + F+ P S+ ++ ADG+ +++ + N

Sbjct: 815 RAGESVSVTSPALVGMTMTMTFSADPRTAVVSTLAAIDNNAKADGTD TNVVRWVVDAN 874

Query: 578 NEFVSGITDLEFIQSGVPVTISPVTENADNYTASVVG 615
 V G++ +G + +PV + + Y + + N
 Sbjct: 875 GNSVPGVSVTFDAGNGAVLAQNPVVTDRNGYAENTLTN 912

tr Q74QZ6 Putative invasin [YP3306] [Yersinia pestis] 3108 AA
align

Score = 428 bits (1100), Expect = e-118
 Identities = 265/703 (37%), Positives = 382/703 (53%), Gaps = 38/703 (5%)

Query: 66 SGNASNITRSMVNDAAANQEVKHWLNRFGTQVNVNFDKKFSLKESSLDWLLPWPYDSASYV 125
 S ASN+ RS V + N + WLN+FGT +V +N D F L S+LD L+P DS S +
 Sbjct: 178 SDAASNMARSAVTNEINASSQQWLNQFGTARVQLNVDSDFKLDNSALDLLVPLKDSSESL 237

Query: 126 FFSQLGIRNKDSRNTLNIGAGVRTFQQSWMYGFNTSYDNDMTGHNHRIGVGAEAWTDYLO 185
 F+QLG+RNKDSRNT+NIGAG+R +Q WMYG NT +DND+TG N R+GVGAE TDYL+
 Sbjct: 238 LFTQLGVRNKDSRNTVNIGAGIRQYQGDWMYGANTFFDNDLTGKNRRRVGVGAEVATDYLK 297

Query: 186 LSANGYFRLNGWHQSRDFADYNERPASGGDIHVKAYLPALPQLGGKLYEQYRGERVALF 245
 SAN YF L GWHQSRDF+ Y+ERPA G DI +AYLPA PQLGGKL YE+YRG+ VALF
 Sbjct: 298 FSANTYFGLTGWHQSRDFSSYDERPADGFDIRTEAYLPAYPQLGGKLMYEKYRGDEVALF 357

Query: 246 GKDNLQSNPYAVTTGLIYTPIPFITLGVDQRMGKSRQHEIQWNLMQDYRLGESFRSQFSP 305
 GKD+ Q +P+AVT G+ YTP+P +T+G + R GK + N+Q++YR+G+ + Q
 Sbjct: 358 GKDDRQKDPHAVTLGVNYTPVPLVTIGAEHREGKGNNNNTSVNVQLNYRMGQPWNDQIDQ 417

Query: 306 AVVAGTRLLAESRYNLVERNPNIVLEYQKQNTIKLAFSPAVALSGLPGQVYSVSAQIQSQS 365
 + VA R LA SRY+LVERN NIVL+Y+KQ I L P +SG G +++AQ++++
 Sbjct: 418 SAVAANRTLAGSRYDLVERNINNIVLDYKKQELIHLVL-PDRISGSGGGAITLTAQVRACY 476

Query: 366 ALQRILWNDAAQWVAAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTGESEAAVNTYTLS 425
 RI W+ AGG P++ + +V LP Y+ + S NT+T+S
 Sbjct: 477 GFSRIEWDATPLENAGGSTSPLTQSSLSVTLFPYQHILRTS-----NTHTIS 523

Query: 426 ATAIDNHGSSNPATLTVIVQQPQFVITSEV--TDDGALADGRTPITVKFTVTNIDSTPV 483
 A A D GN+SN A ++ V +P+ ++ S + T D A A+G TV+ TVT+ D P+
 Sbjct: 524 AVAYDAQGNASNAVTSIEVTRPETMVISHLATIDNATANGIATNTVQATVTDGDGQPI 583

Query: 484 AEQEGVITTSNGALPSKVTKKTDAGQVISIALTSFTVGVSVVTLDIQQQATVDVRFVAV- 542
 Q + A S +T A G S LT GVS V++ + +VD F
 Sbjct: 584 IGQLINFAVNTQATLSTTEARTGANGTASTTLTHTVSGVSRVSVTLGSSSRVDTTFVAD 643

Query: 543 -LPPDVTNSSFNVSPSDIVADGSMQSILTFVPRNKNNEFVSGITDLEFIQSGVPVTISP 601
 ++T ++ V+ +D VA+GS +++ + V+ + + +G V V
 Sbjct: 644 ESTAEITAANLTVTTNDSVANGSDTNVVRKVTDAYTNAVANQSVIFSASNGATVIDQTV 703

Query: 602 TENADNYTASVVGNSVGDDVD-ITPQVGGESLDLLQKRITLYPVPKITGINVNGEQFATDK 660
 NA+ S + N+ V +T +GG+S Q T P V A
 Sbjct: 704 ITNAEGIADSTLTNTTAGVSVVTATLGGQS---QQVDTTFKPGSTAAISLVKLADRAVAD 760

Query: 661 GFPKTTFNKATFQLVMNDDVAN-----NTQYDWTSSYAASAP-VDNQGKVNIAV---K 709
 G ++ Q+V+ D N + Q D + AS P G +N + +
 Sbjct: 761 G-----IDQNEIQVVLRDGTGNAVNPVPMISIQADNGAIVVASTPNTGVDGTINATFTNLR 815

Query: 710 TYGSTVTVTAKSKKFPSYATATYQFKPNLWVFSGTMSLQSSVEA 752

S V+VT+ + + T T+ P V S ++ ++ +A

Sbjct: 816 AGESVSVTSPALVGMTMTMTFSADPRTAVVSTLAAIDNNAKA 858

Score = 122 bits (305), Expect = 4e-26

Identities = 123/477 (25%), Positives = 199/477 (40%), Gaps = 28/477 (5%)

Query: 374 DAQWVAAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTGESEAAVNTYTLSATAIDNHG 433

DA GG+ + SAT+ + ++ +V + S A + ++ T + N+

Sbjct: 2643 DANQNPVGGQQVAFSATNEVTLTESNGSISTPEGSVLLSVTSTQA-GVHPITGTLVSNNY 2701

Query: 434 NSSNPATLTVIVQQPQFVITSEVTDGALADGRTPITVKFTVTNIDSTPVAEQEGVITTS 493

+ A Q + T V D+ ALADG T V+ V + VA+ T +

Sbjct: 2702 TDTFGAAFIANKNTAQ-LSTLMVVDNNALADGVTRNQVRAHVVDSTGNSVADMAVTFITAN 2760

Query: 494 NGALPSKVTKKTDAGQVISIALTSFTVGVSVVT--LDIQGQQATVDVRFVAVLPPDVTNSS 551

GA SKVT TD G LT+ VGV+VVT L G TVD F P + +

Sbjct: 2761 RGAQLSKVTVLTDNNGDAVNTLTNSLVGVTVVTAKLGTAGTPLTVDVTFVITAGP--LATLT 2818

Query: 552 FNVSPSDIVADGSMQSILTFVPRNKNEFVSGITDLEFIQSGVPVTISP-VTENADNYTA 610

+ ++ AD S + + ++ + + G +G +T + NA+

Sbjct: 2819 LVTTVNNAFADNSATNTVQATLKDVSGNPVGEVVAFAASNGATITATDGGVSNANGIVL 2878

Query: 611 SVVGNSVGDVDITPQVGGESLDLLQKRITLYPVPKITGINVNGEQFATDKGFPKTTFNKA 670

+ + N V V L + T + K + VNG F D GFP T F A

Sbjct: 2879 ATLTNGTAGVS---TVTATITETLTETDTTFIAMKNLDVTVNGTTFNGDAGFPTTGFGVA 2935

Query: 671 TFQLVMNDDVANNTQYDWTSSYAASAPVDNQGV--NIAKYTYGSTVTVTAKSKKFPSYT 728

TF++ D N+ YDW+SS A V G V N + T T+T++A K S

Sbjct: 2936 TFKVNSGGD---NSLYDWSSAPALVSVSGDGVVTFNAVFPTGTPTITISATPKGGGS-P 2991

Query: 729 ATYQFKPNLWVFSGTMSLQSSVEASRNCQRTDF-----TALIESARASNGSRSPDGTWLG 783

+Y F+ N W + + + +A +C+ + T + +A +G R+ G LW

Sbjct: 2992 LSYSFRVNQWFINNNGATLNRADAITHCENVGYTMPTSTQVTNAATWMSGKRAV-GNLWS 3050

Query: 784 EWGSLATYDSAEW-PSGNYWTKKT--STDFVTMDMTTGDIPSA---ATAYPLCAEP 834

EWG + Y + W P+ +W ++ + + ++TG + T A + +C P

Sbjct: 3051 EWGDFSAYTAPGWVPAEFFWLSNNHDASTALAIGLSTGTLTMTMGDFMAITHVMCTRP 3107

Score = 60.1 bits (144), Expect = 2e-07

Identities = 54/203 (26%), Positives = 86/203 (41%), Gaps = 7/203 (3%)

Query: 418 AVNTYTLSATAIDNH--GNSSNPATLTVIVQQPQFVITSE---VTDDGALADGRTPITVK 472

A T+TL+ T++ GN T I + I + +T + ALADG +

Sbjct: 2078 ATLTHTLAGTSVVVTARVGNRVQSKDTTFIADRTTATIRASDLTITRNNALADGVATNAAR 2137

Query: 473 FTVTNIDSTPVAEQEGVITTSNGALPSKVTKKTDAGQVISIALTSFTVGVSVVTLDI--Q 530

VT+ + PV T+ NGAL + + TD+ G S T T G+S VT I

Sbjct: 2138 VIVTDANGNPVPSMFVGYTSDNGALLTPTSGMTDSSGTFSTTFHTTAGISKVTAIVTM 2197

Query: 531 GQQATVDVRFVAVLPPDVTNSSFNVSFSDIVADGSMQSILTFVPRNKNEFVSGITDLEFI 590

G T D F S V +D +A+ S ++I+ ++ + V+G+

Sbjct: 2198 GISQTKDAVFIADRSTAHVSELIVVKNDLANNSDRNIVQAHIKDAHGNVVTGMNVNFSA 2257

Query: 591 QSGVPVTISPVTENADNYTASVV 613

V +T + VT N+ Y + +

Sbjct: 2258 TENVTLTANTVTTNSQGYAENTL 2280

Score = 56.6 bits (135), Expect = 2e-06

Identities = 63/250 (25%), Positives = 93/250 (37%), Gaps = 10/250 (4%)

Query: 373 NDAQWVAAGGKLIPVSATDYNVVLPPYKPMAPASRTVGKTGESEAAVNTYTLSATAIDNH 432

N Q V + PV T VV A + +G TG A T T + N

Sbjct: 1155 NSVQAVVSDSDGNPV--TGAADVVFSSANATAQITTVIGTTGADGIATATLTNTVAGTSNV 1212

Query: 433 G---NSSNPATLTVIVQQPQFVITSEVTDDGALADGRTPITVKFTVTNIDSTPVAEQEGV 489

++ N T V IT +GA+ADG V V + + P+ V

Sbjct: 1213 VATIDTVNANIDTAFVAGAVATITLTAPVNGAVADGADTNQVDALVEDANGNPITGAADV 1272

Query: 490 ITTSNGALPSKVTKKTDAGQGVISIALTSFTVGVSVVTLDIQQQATVDVRFVAVLPPDVTN 549

+++NGA T T GV S LT G S V + A +D F +P V

Sbjct: 1273 FSSANGATILSSTMNTGVNGVASTLLTHTVAGTSNVVATVDTVNANIDTAF--VPGAVAT 1330

Query: 550 SSFNVSPSIVADGSMQSILTFVPRNKNEFVSGITDLEFIQSGVPVTISPV--TENADN 607


+ + VADG+ + + V + V+G + F + I+ V T AD

Sbjct: 1331 ITLTTPVNGAVADGANSNSVQAVVSDSEGNVAGAA-VVFSSANATAQITTVIGTTGADG 1389

Query: 608 YTASVVGNSV 617

+ + N+V

Sbjct: 1390 IATATLTNTV 1399

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TrEMBL Release 27.5 of 13-Sep-2004

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Search in Swiss-Prot: There are matches to 11 out of 158316 entries

[INVA_YEREN \(P19196\)](#)

Invasin. [Yersinia enterocolitica](#)

[INVA_YERPS \(P11922\)](#)

Invasin. - *Yersinia pseudotuberculosis*

[IPAA_SHIFL \(P18010\)](#)

Invasin ipaA (70 kDa antigen). {GENE: Name=ipaA; OrderedLocusNames=CP0125} - [Shigella flexneri](#)

[IPAB_SHIDY \(Q03945\)](#)

Invasin ipaB (62 kDa antigen). {GENE: Name=ipaB} - *Shigella dysenteriae*

[IPAB_SHIFL \(P18011\)](#)

Invasin ipaB (62 kDa antigen). {GENE: Name=ipaB; OrderedLocusNames=CP0128} - *Shigella flexneri*

[IPAC_SHIDY \(Q03946\)](#)

Invasin ipaC (42 kDa antigen). {GENE: Name=ipaC} - *Shigella dysenteriae*

[IPAC_SHIFL \(P18012\)](#)

Invasin ipaC (42 kDa antigen). {GENE: Name=ipaC; OrderedLocusNames=CP0127} - *Shigella flexneri*

[IPAD_SHIDY \(Q03947\)](#)

Invasin ipaD (37 kDa membrane antigen). {GENE: Name=ipaD} - *Shigella dysenteriae*

[IPAD_SHIFL \(P18013\)](#)

Invasin ipaD (36 kDa membrane antigen). {GENE: Name=ipaD; OrderedLocusNames=CP0126} - *Shigella flexneri*

[YADA_YEREN \(P31489\)](#)

Invasin precursor (Outer membrane adhesin). {GENE: Name=yadA; Synonyms=yopA, invA, yop1} - *Yersinia enterocolitica*

[YADA_YERPS \(P10858\)](#)

Invasin precursor (Outer membrane adhesin). {GENE:Name=yadA; Synonyms=yopA, invA, yop1} - *Yersinia pseudotuberculosis*

Search in TrEMBL: There are matches to 45 out of 1400820 entries

O07390

Invasin 1 {GENE:Name=inv1} - *Mycobacterium avium*

O07391

Invasin 2 {GENE:Name=inv2} - *Mycobacterium avium*

O84129

Predicted polysaccharide hydrolase-invasin repeat family {GENE:Name=ydhO;
OrderedLocusNames=CT127} - *Chlamydia trachomatis*

O84606

Invasin repeat family phosphatase {GENE:Name=papQ; OrderedLocusNames=CT601} -
Chlamydia trachomatis

O84764

Muramidase (Invasin repeat family) {GENE:Name=nlpD; OrderedLocusNames=CT759} -
Chlamydia trachomatis

Q47380

Invasin - *Escherichia coli*

Q56889

Invasin {GENE:Name=invA} - *Yersinia enterocolitica*

Q56937

Invasin {GENE:Name=inv} - *Yersinia pestis*

Q6T8F2

Putative invasin-like protein (Fragment) - *Chlamydia suis*

Q6T8F6

TetR(C)-invasin fusion protein (Fragment) - *Chlamydia suis*

Q6T8F7

Invasin-like protein (Fragment) - *Chlamydia suis*

Q6T8G9

Invasin-like protein (Fragment) - *Chlamydia suis*

Q74QZ6

Putative invasin {GENE:OrderedLocusNames=YP3306} - *Yersinia pestis*

Q7A8L6

Putative invasin {GENE:OrderedLocusNames=ECs5290} - *Escherichia coli* O157:H7

Q7AGX0

Adhesin/invasin-like protein {GENE:OrderedLocusNames=ECs0548} - *Escherichia coli*
O157:H7

Q7AHB0

Putative invasin {GENE:OrderedLocusNames=ECs0336} - *Escherichia coli* O157:H7

Q7N592

Similar to putative invasin and adhesin {GENE:OrderedLocusNames=plu2064} - *Photobacterium*
luminescens (subsp. *laumondii*)

Q83T27

Invasin-like protein {GENE:OrderedLocusNames=t1573} - *Salmonella typhi*

Q8EFM1

Invasin domain protein {GENE:OrderedLocusNames=SO1949} - *Shewanella oneidensis*

Q8FY77

Q8KH85
Intimin/invasin family protein {GENE:OrderedLocusNames=BR2009} - *Brucella suis*

Q8KHF7
Putative adhesin/invasin - *Neisseria meningitidis*

Q8KHP5
Putative adhesin/invasin - *Neisseria meningitidis*

Q8KI42
Putative adhesin/invasin - *Neisseria meningitidis*

Q8KUJ1
Putative adhesin/invasin - *Neisseria meningitidis*

Q8KUJ6
Putative adhesin/invasin - *Neisseria meningitidis*

Q8KWG5
Putative invasin protein {GENE:Name=agg3B} - *Escherichia coli* [Plasmid pAA-like]

Q8RBD9
Soluble lytic murein transglycosylase and related regulatory proteins (Some contain LysM/invasin domains) {GENE:Name=MltE2; OrderedLocusNames=TTE0883} - *Thermoanaerobacter tengcongensis*

Q8RBE4
Soluble lytic murein transglycosylase and related regulatory proteins (Some contain LysM/invasin domains) {GENE:Name=MltE; OrderedLocusNames=TTE0876} - *Thermoanaerobacter tengcongensis*

Q8RQ63
Putative adhesin/invasin {GENE:Name=Aa32-1-2} - *Actinobacillus actinomycetemcomitans* (*Haemophilus actinomycetemcomitans*)

Q8VM53
Putative invasin {GENE:Name=pagN} - *Salmonella enterica* IIIb 50:k:z

Q8XB95
Putative invasin {GENE:OrderedLocusNames=z5932} - *Escherichia coli* O157:H7

Q8Z795
Invasin-like protein {GENE:OrderedLocusNames=STY1395} - *Salmonella typhi*

Q8Z7G3
Putative invasin {GENE:OrderedLocusNames=STY1284, t1677} - *Salmonella typhi*

Q8ZA73
Putative invasin (Hypothetical) {GENE:OrderedLocusNames=YPO3944, y3884} - *Yersinia pestis*

Q8ZP33
Putative invasin {GENE:Name=yehP; OrderedLocusNames=STM1768} - *Salmonella typhimurium*

Q8ZP78
Homology to invasin C of *Yersinia*; intimin {GENE:OrderedLocusNames=STM1669} - *Salmonella typhimurium*

Q9AM40
Invasin (Fragment) {GENE:Name=inv} - *Yersinia pseudotuberculosis*

Q9JSH2
Polysaccharide hydrolase-invasin repeat family {GENE:Name=ydhO} - *Chlamydia pneumoniae* (*Chlamydophila pneumoniae*)

Q9JXK7
Adhesin/invasin, putative {GENE:OrderedLocusNames=NMB1994} - *Neisseria meningitidis* (serogroup B)

Q9KK70

Putative invasin 996A009 (Fragment) - Mycobacterium avium
[Q9L574](#)

Invasin-like SivH {GENE:Name=sivH} - Salmonella typhi
[Q9X4L4](#)

Invasin homolog AafB {GENE:Name=aafB} - Escherichia coli
[Q9Z704](#)

Muramidase (Invasin repeat family) (Hypothetical protein CP0964) (Cell wall hydrolase)
{GENE:Name=nlpD; Synonyms=lytE; OrderedLocusNames=CP0964, CPn0902, CpB0934} -
Chlamydia pneumoniae (Chlamydophila pneumoniae)

[Q9Z8T9](#)
Polysaccharide Hydrolase-Invasin Repeat Family (NLP/P60 family protein) (P60)
{GENE:Name=ydhO; OrderedLocusNames=CP0517, CPn0245, CpB0252} - Chlamydia
pneumoniae (Chlamydophila pneumoniae)

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Entry information

Entry name	Q56889
Primary accession number	Q56889
Secondary accession numbers	None
Entered in TrEMBL in	Release 01, November 1996
Sequence was last modified in	Release 01, November 1996
Annotations were last modified in	Release 26, March 2004
Name and origin of the protein	
Protein name	Invasin
Synonyms	None
Gene name	Name: invA
From	<u>Yersinia enterocolitica</u> [TaxID: 630]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Gammaproteobacteria</u> ; <u>Enterobacteriales</u> ; <u>Enterobacteriaceae</u> ; <u>Yersinia</u> .

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=W1024;

MEDLINE=94195100;PubMed=7511772 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

[Pepe J.C.](#), [Badger J.L.](#), [Miller V.L.](#);

"Growth phase and low pH affect the thermal regulation of the *Yersinia enterocolitica* inv gene."; *Mol. Microbiol.* 11:123-135(1994).

[2] SEQUENCE FROM NUCLEIC ACID.

STRAIN=W1024;

MEDLINE=98048470;PubMed=9387224 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

[Fauconnier A.](#), [Allaoui A.](#), [Campos A.](#), [Van Elsen A.](#), [Cornelis G.R.](#), [Bollen A.](#);

"Flagellar flhA, flhB and flhE genes, organized in an operon, cluster upstream from the inv locus in *Yersinia enterocolitica*."; *Microbiology* 143:3461-3471(1997).

Comments

None

Cross-references

EMBL [Z48169](#); [CAA88188.1](#); -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
 PIR [S54216](#); [S54216](#).
 HSSP [P11922](#); [1CWV](#). [[HSSP ENTRY](#) / [PDB](#)]
 GO [GO:0007155](#); Biological process: cell adhesion (*inferred from electronic annotation*).
 QuickGo [view](#).
 InterPro [IPR003344](#); [Big_1](#).
[IPR003535](#); [Intimin](#).
[IPR008964](#); [Invasin_intimin](#).
[Graphical view of domain structure](#).
 Pfam [PF02369](#); [Big_1](#); [1](#).
[Pfam graphical view of domain structure](#).
 PRINTS [PR01369](#); [INTIMIN](#).
 ProDom [\[Domain structure / List of seq. sharing at least 1 domain\]](#)
 HOBACGEN [\[Family / Alignment / Tree\]](#)
 ProtoMap [Q56889](#).
 PRESAGE [Q56889](#).
 ModBase [Q56889](#).
 SMR [Q56889](#); [C817F6D7766184E3](#).
 SWISS-2DPAGE [Get region on 2D PAGE](#).
 UniRef View cluster of proteins with at least [50%](#) / [90%](#) identity.

Keywords

None

Features

None

Sequence information

Length: **835** Molecular weight: **91367** CRC64: **C817F6D7766184E3** [This is a checksum on the
 AA Da sequence]

10	20	30	40	50	60
MYSFFNTLTV	TKIISRLILS	IGLIFGIFTY	GFSQQNYFNS	EALENPAEHN	EAFNKIISTG
70	80	90	100	110	120
TSLAVSGNAS	NITRSMVND	ANQEVKHWLN	RFGTTQVNVN	FDKKFSLKES	SLDWLLPWYD
130	140	150	160	170	180
SASYVFFSQL	GIRNKDSRNT	LNIGAGVRTF	QQSWMYGFNT	FYDNDMTGHN	HRIGVGAEAW
190	200	210	220	230	240
TDYLQLSANG	YFRLNGWHQS	RDFVDYNERP	ASGGDIHVKA	YLPALPQLGG	KLKYEQYRGE
250	260	270	280	290	300
RVALFGKDNL	QSNPYAVTTG	LIYTPIPFIT	LGVDQRMGKS	RQHEIQWNLQ	MDYRLGESFR

```

      310           320           330           340           350           360
      |           |           |           |           |           |
SQFSPAVVAG TRLLAESRYN LVERNPNIVL EYQKQNTIKL AFSPAVLSGL PGQVYSVSAQ

      370           380           390           400           410           420
      |           |           |           |           |           |
IQSQSALQRI LWDDAQWIAV GGKLIPVSAT NYNVVLPPYK PMAPASRTVG KTGESEAAVN

      430           440           450           460           470           480
      |           |           |           |           |           |
TYTLSATAID NHGNSSNPAT LTVIVQQPQF VITSEVTDDG ALADGRTPIT VKFTVTNIDG

      490           500           510           520           530           540
      |           |           |           |           |           |
TPVAEQEGVI TTSNGALPSK VTKKTDAGV ISIALTSFTV GGSVVTLDIQ GQQATVDVRF

      550           560           570           580           590           600
      |           |           |           |           |           |
AVLPPDVTNS SFNVSPSDIV ADGSMQSILT FVPRNKNEF VSGITDLEFI QSGVPVTISP

      610           620           630           640           650           660
      |           |           |           |           |           |
VTENADNYTA SVVGNSVGDV DITPQVGES LDLLQKRITL YPIPKITSIA VNGEQFATDK

      670           680           690           700           710           720
      |           |           |           |           |           |
GFPKTTFNKA TFQLVMNDDV ANNTQYDWT S Y AASAPVDN QGKVNIAYKT YGSTVTVTAK

      730           740           750           760           770           780
      |           |           |           |           |           |
SKKFPSYTAT YQFKPNLWVF SGTMSLQSSI EASRNCQRTD FTALIESARA SNGSRSPDGT

      790           800           810           820           830
      |           |           |           |           |
LWGEWGSLAT YDSAEWPSGN YWTKKTSTDF VTMDMTTGAI PTSAATAYPL CAEPQ

```

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Entry information

Entry name **YADA_YEREN**
 Primary accession number **P31489**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 26, July 1993
 Sequence was last modified in Release 26, July 1993
 Annotations were last modified in Release 44, July 2004

Name and origin of the protein

Protein name **Invasin [Precursor]**
 Synonym **Outer membrane adhesin**
 Gene name **Name: yadA**
 Synonyms: yopA, invA, yop1
 From Yersinia enterocolitica [TaxID: 630]
 Encoded on Plasmid pYV.
 Taxonomy Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=6471/76 / Serotype O:3;

MEDLINE=95020586;PubMed=7934875 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

[Tamm A.](#), [Tarkkanen A.](#), [Korhonen T.K.](#), [Kuusela P.](#), [Toivanen P.](#), [Skurnik M.](#);

"Hydrophobic domains affect the collagen-binding specificity and surface polymerization as well as the virulence potential of the YadA protein of *Yersinia enterocolitica*.";

Mol. Microbiol. 10:995-1011(1993).

Comments

- **FUNCTION:** Invasin is a protein that allows enteric bacteria to penetrate cultured mammalian cells. The entry of invasin in the cell is mediated by binding several beta-1 chain integrins. This protein is an adhesin forming a fibrillar matrix on the cell surface.
- **SUBCELLULAR LOCATION:** Outer membrane.

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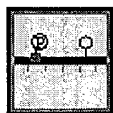
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Cross-references

EMBL [X13882](#); [CAA32086.1](#); -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
 PIR [S04912](#); [S04912](#).
[IPR008126](#); Adhesion.
[IPR008640](#); Hep_Hag.
 InterPro [IPR008635](#); HIM.
[IPR005594](#); YadA_C.
[Graphical view of domain structure](#).
[PF05658](#); Hep_Hag; 4.
 Pfam [PF05662](#); HIM; 1.
[PF03895](#); YadA; 1.
[Pfam graphical view of domain structure](#).
 PRINTS [PR01756](#); OMADHESIN.
 ProDom [\[Domain structure / List of seq. sharing at least 1 domain\]](#)
 HOBACGEN [\[Family / Alignment / Tree\]](#)
 BLOCKS [P31489](#).
 ProtoNet [P31489](#).
 ProtoMap [P31489](#).
 PRESAGE [P31489](#).
 DIP [P31489](#).
 ModBase [P31489](#).
 SMR [P31489](#); [AC12EF68C657DAC0](#).
 SWISS-2DPAGE [Get region on 2D PAGE](#).
 UniRef [View cluster of proteins with at least 50% / 90% identity](#).

Keywords

Outer membrane; Plasmid; Signal; Virulence.

Features

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Key	From	To	Length	Description
SIGNAL	1	25	25	
CHAIN	26	455	430	Invasin.

Sequence information

Length: **455 AA** [This is the length of the unprocessed precursor]
 Molecular weight: **47136 Da** [This is the MW of the unprocessed precursor]

CRC64: **AC12EF68C657DAC0** [This is a checksum on the sequence]

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70	80	90	100	110	120

```

      |      |      |      |      |      |
GGLNASAKGI HSAIGATAE AAKGAAVAVG AGSIATGVNS VAIGPLSKAL GDSAVTYGAA
      |      |      |      |      |      |
    130    140    150    160    170    180
      |      |      |      |      |      |
STAQKDGVAI GARASTSDTG VAVGFNSKAD AKNSVAIGHS SHVAANHGYG IAIGDRSKTD
      |      |      |      |      |      |
    190    200    210    220    230    240
      |      |      |      |      |      |
RENSVSIGHE SLNRQLTHLA AGTKDTPDAVN VAQLKKEIEK TQENTNKRSA ELLANANAYA
      |      |      |      |      |      |
    250    260    270    280    290    300
      |      |      |      |      |      |
DNKSSSVLGI ANNYTDSKSA ETLENARKEA FAQSKDVLNM AKAHSNSVAR TTLETAEHA
      |      |      |      |      |      |
    310    320    330    340    350    360
      |      |      |      |      |      |
NSVARTTLET AEEHANKKSA EALASANVYA DSKSSHTLKT ANSYTDVTVS NSTKKAIRES
      |      |      |      |      |      |
    370    380    390    400    410    420
      |      |      |      |      |      |
NQYTDHKFRQ LDNRLDKLDT RVDKGLASSA ALNSLFQPYG VGKVNFTAGV GGYRSSQALA
      |      |      |      |      |      |
    430    440    450
      |      |      |
IGSGYRVNEN VALKAGVAYA GSSDVMYNAS FNIEW

```

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Entry information

Entry name	YADA_YERPS
Primary accession number	P10858
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 11, July 1989
Sequence was last modified in	Release 11, July 1989
Annotations were last modified in	Release 44, July 2004
Name and origin of the protein	
Protein name	Invasin [Precursor]
Synonym	Outer membrane adhesin
Gene name	Name: yadA
	Synonyms: yopA, invA, yop1
From	<u>Yersinia pseudotuberculosis</u> [TaxID: 633]
Encoded on	Plasmid pIB1.
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Gammaproteobacteria</u> ; <u>Enterobacteriales</u> ; <u>Enterobacteriaceae</u> ; <u>Yersinia</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=YPIII;
 DOI=10.1038/334522a0;MEDLINE=88302441;PubMed=3043229 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#),
[Japan](#)]
Rosqvist R., Skurnik M., Wolf-Watz H.;
 "Increased virulence of *Yersinia pseudotuberculosis* by two independent mutations.";
 Nature 334:522-525(1988).
- [2] SEQUENCE FROM NUCLEIC ACID.
STRAIN=YPIII;
 MEDLINE=89343638;PubMed=2761389 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Skurnik M., Wolf-Watz H.;
 "Analysis of the yopA gene encoding the Yop1 virulence determinants of *Yersinia* spp.";
 Mol. Microbiol. 3:517-529(1989).

Comments

- **FUNCTION:** Invasin is a protein that allows enteric bacteria to penetrate cultured mammalian cells. The entry of invasin in the cell is mediated by binding several beta-1 chain integrins. This protein is an adhesin forming a fibrillar matrix on the cell surface.
- **SUBCELLULAR LOCATION:** Outer membrane.

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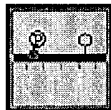
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Cross-references

EMBL X13883; CAA32088.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
 PIR S04534; S04534.
 IPR008126; Adhesion.
 IPR008640; Hep_Hag.
 InterPro IPR008635; HIM.
 IPR005594; YadA_C.
Graphical view of domain structure.
 PF05658; Hep_Hag; 4.
 Pfam PF05662; HIM; 1.
 PF03895; YadA; 1.
Pfam graphical view of domain structure.
 PRINTS PR01756; OMADHESIN.
 ProDom [Domain structure / List of seq. sharing at least 1 domain]
 HOBACGEN [Family / Alignment / Tree]
 BLOCKS P10858.
 ProtoNet P10858.
 ProtoMap P10858.
 PRESAGE P10858.
 DIP P10858.
 ModBase P10858.
 SMR P10858; EE2C55FB12B183D4.
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 UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Outer membrane; Plasmid; Signal; Virulence.

Features

Feature table viewer

Key	From	To	Length	Description
SIGNAL	1	25	25	
CHAIN	26	434	409	Invasin.

Sequence information

Length: **434 AA** [This is the length of the unprocessed
 Molecular weight: **45054 Da**
 [This is the MW of the

CRC64: **EE2C55FB12B183D4** [This is a checksum on the sequence]

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      70      80      90     100     110     120
      |      |      |      |      |      |
ILRQENPKLP PRGPQGPEKK RARLAEAIQP QVLGAGGLNA RAKDPYSIAI GATAEAAKPA
     130     140     150     160     170     180
      |      |      |      |      |      |
AVAVGSGSIA TGVNSVAIGP LSKALGDSAV TYGASSTAQK DGVAIGARAS ASDTGVAVGF
     190     200     210     220     230     240
      |      |      |      |      |      |
NSKVDAQNSV AIGHSSHVAA DHGYSIAIGD HSKTDRENSV SIGHESLNRQ LTHLAAGTED
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      |      |      |      |      |      |
TDAVNVAQLK KEMAETLENA RKETLAQSDN VLDAKKHSN SVARTTLETA EEHANKKSAE
     310     320     330     340     350     360
      |      |      |      |      |      |
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     370     380     390     400     410     420
      |      |      |      |      |      |
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     430
      |
SSNVMYNASF NIEW

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NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
1,568,464 sequences; 501,960,298 total letters

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<input type="checkbox"/>	tr	Q7WP64	Autotransporter [BB0821] [Bordetella bronchiseptica (A...	45	0.003
<input type="checkbox"/>	tr	Q6G430	Hypothetical protein [BH05490] [Bartonella henselae (R...	44	0.008
<input type="checkbox"/>	tr	Q7W7D4	Putative autotransporter [bapC] [Bordetella parapertus...	44	0.008
<input type="checkbox"/>	tr	Q9JMS5	YcbB protein [ycbB] [Escherichia coli]	44	0.013
<input type="checkbox"/>	tr	Q9XD84	TibA [tibA] [Escherichia coli]	43	0.017
<input type="checkbox"/>	tr	Q6G428	Hypothetical protein [BH05510] [Bartonella henselae (R...	42	0.029
<input type="checkbox"/>	tr	Q83JR2	Exported serine protease SigA [sigA] [Shigella flexneri]	42	0.029
<input type="checkbox"/>	tr	Q9L8L1	Exported serine protease SigA [sigA] [Shigella flexner...	42	0.029
<input type="checkbox"/>	tr	Q7C013	Serine protease [sigA] [Shigella flexneri]	42	0.029
<input type="checkbox"/>	tr	Q8UJW1	Autotransporter protein [yapE] [Agrobacterium tumefaci...	40	0.14
<input type="checkbox"/>	tr	Q7D396	AGR_pAT_528p [AGR_pAT_528] [Agrobacterium tumefaciens ...	40	0.14
<input type="checkbox"/>	tr	Q7WK90	Autotransporter [phg] [Bordetella bronchiseptica (Alca...	40	0.19
<input type="checkbox"/>	tr	Q7W8X9	Autotransporter [phg] [Bordetella parapertussis]	40	0.19
<input type="checkbox"/>	tr	Q84GK0	Secreted autotransporter protein EatA [eatA] [Escheric...	40	0.19
<input type="checkbox"/>	tr	Q8UJX1	Autotransporter protein [bapA] [Agrobacterium tumefaci...	39	0.25
<input type="checkbox"/>	tr	Q7D3A2	AGR_pAT_511p [AGR_pAT_511] [Agrobacterium tumefaciens ...	39	0.25
<input type="checkbox"/>	tr	Q6MTD5	Hypothetical transmembrane protein [MSC_0473] [Mycopla...	39	0.32
<input type="checkbox"/>	sp	P45386	IGA4_HAEIN Immunoglobulin A1 protease precursor (EC 3....	39	0.42
<input type="checkbox"/>	tr	Q9Z5R3	Phg protein (Autotransporter) [phg] [Bordetella pertus...	38	0.55
<input type="checkbox"/>	tr	Q6KD18	Antigen 43 precursor Sap [sap] [Escherichia coli]	38	0.71
<input type="checkbox"/>	tr	Q8FDW4	Accreted auto transpoter toxin [sat] [Escherichia coli...	37	1.2

Graphical overview of the alignments

[Click here](#)

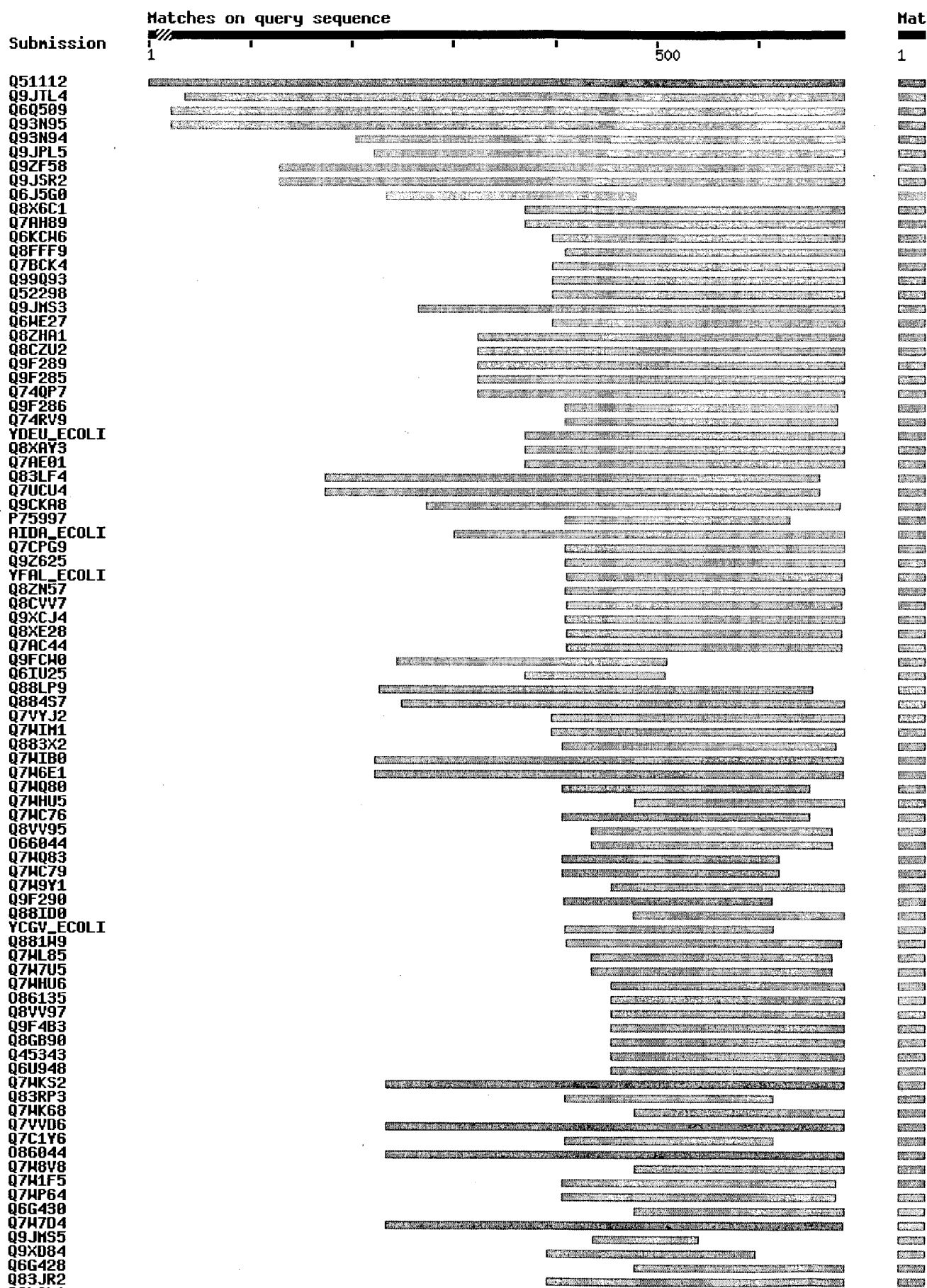
to resubmit your query after masking regions matching PROSITE profiles
or Pfam HMMs

([?](#) Help) (use ScanProsite for more details about PROSITE matches)

Profile hits

Pfam hits

Autotransporter



Alignments

tr Q51112 Similar to *Shigella flexneri* VirG protein (Fragment) 682
[*Neisseria* AA
meningitidis] align

Score = 1367 bits (3538), Expect = 0.0
Identities = 669/682 (98%), Positives = 669/682 (98%)

Query: 1 QRKIYYETRXXXXXXXXXXXXXIVSLFFSILYTSPLLAVDYVYDKTKLTNDEITRLKKLR 60
QRKIYYETR IVSLFFSILYTSPLLAVDYVYDKTKLTNDEITRLKKLR
Sbjct: 1 QRKIYYETR SKQASKQKFKKSFIVSLFFSILYTSPLLAVDYVYDKTKLTNDEITRLKKLR 60

Query: 61 DKTSEYWKKETYLTEDNPKVPPFPALYPRTYQFENINNSKKISFYDQEYTEGYLVGFAR 120
DKTSEYWKKETYLTEDNPKVPPFPALYPRTYQFENINNSKKISFYDQEYTEGYLVGFAR
Sbjct: 61 DKTSEYWKKETYLTEDNPKVPPFPALYPRTYQFENINNSKKISFYDQEYTEGYLVGFAR 120

Query: 121 GLGVAKRNGDTEEQIRKYFKECFNSNTKIRDYSTCQAEKFGSHPLIVKSHIFSLGPKIKN 180
GLGVAKRNGDTEEQIRKYFKECFNSNTKIRDYSTCQAEKFGSHPLIVKSHIFSLGPKIKN
Sbjct: 121 GLGVAKRNGDTEEQIRKYFKECFNSNTKIRDYSTCQAEKFGSHPLIVKSHIFSLGPKIKN 180

Query: 181 SHINSEILSVGNYTEWANQVIHHIENYVSFAAHLYSGLDPFHYIEVTDNSHVIGQTISLD 240
SHINSEILSVGNYTEWANQVIHHIENYVSFAAHLYSGLDPFHYIEVTDNSHVIGQTISLD
Sbjct: 181 SHINSEILSVGNYTEWANQVIHHIENYVSFAAHLYSGLDPFHYIEVTDNSHVIGQTISLD 240

Query: 241 EFRLNSLWEPRWDSNVGKLTNNADIRFNTKSESLLVKEDYAGGARFRFAYDPKEAKNT 300
EFRLNSLWEPRWDSNVGKLTNNADIRFNTKSESLLVKEDYAGGARFRFAYDPKEAKNT
Sbjct: 241 EFRLNSLWEPRWDSNVGKLTNNADIRFNTKSESLLVKEDYAGGARFRFAYDPKEAKNT 300

Query: 301 ALIFEKNVTGTSDIIFENPIDDLKSLDGHQIIVKNGTADKHAFLRSGKHQKGIYTLSQLQ 360
ALIFEKNVTGTSDIIFENPIDDLKSLDGHQIIVKNGTADKHAFLRSGKHQKGIYTLSQLQ
Sbjct: 301 ALIFEKNVTGTSDIIFENPIDDLKSLDGHQIIVKNGTADKHAFLRSGKHQKGIYTLSQLQ 360

Query: 361 RPEGFLPKCKNAMIWRFMHNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSN 420
RPEGFLPKCKNAMIWRFMHNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSN
Sbjct: 361 RPEGFLPKCKNAMIWRFMHNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSN 420

Query: 421 QWVQGKTAPVEGYRKGVLGGVFTWQNESNQLSIGLMGGQAEQRSTFHNPDNDLTTGN 480
QWVQGKTAPVEGYRKGVLGGVFTWQNESNQLSIGLMGGQAEQRSTFHNPDNDLTTGN
Sbjct: 421 QWVQGKTAPVEGYRKGVLGGVFTWQNESNQLSIGLMGGQAEQRSTFHNPDNDLTTGN 480

Query: 481 VKGFGAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTEDGTERFTSKGITASIEAGYN 540
VKGFGAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTEDGTERFTSKGITASIEAGYN
Sbjct: 481 VKGFGAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTEDGTERFTSKGITASIEAGYN 540

Query: 541 ALLAEHFTKKGNLSRVYLQPQAQLTYLGVNGKFSSENHVNLLGSRQLQTRVGQAKAQ 600
ALLAEHFTKKGNLSRVYLQPQAQLTYLGVNGKFSSENHVNLLGSRQLQTRVGQAKAQ
Sbjct: 541 ALLAEHFTKKGNLSRVYLQPQAQLTYLGVNGKFSSENHVNLLGSRQLQTRVGQAKAQ 600

Query: 601 FSLYKNIAIEPFAAVNALYHNKPFVEMDGERRVINNKTAIESQLGVAVKIKSHLTQAT 660
FSLYKNIAIEPFAAVNALYHNKPFVEMDGERRVINNKTAIESQLGVAVKIKSHLTQAT
Sbjct: 601 FSLYKNIAIEPFAAVNALYHNKPFVEMDGERRVINNKTAIESQLGVAVKIKSHLTQAT 660

Query: 661 FNRQTGKHHQAKQGALNLQWTF 682
FNRQTGKHHQAKQGALNLQWTF
Sbjct: 661 FNRQTGKHHQAKQGALNLQWTF 682

tr Q9JTL4 Putative virulence associated protein [NMA1725] [Neisseria 642 AA
meningitidis (serogroup A)]

align

Score = 1043 bits (2698), Expect = 0.0

Identities = 529/650 (81%), Positives = 568/650 (87%), Gaps = 12/650 (1%)

Query: 37 LAVDYVYDKTKLTNDEITRLKKLRDKTSEYWKKETYLLITEDNPKVPPFPALYPRTY--QF 94
+AVDYVYDKTKLT+DEITRLKKLRD+ SEYWK+ETY I +N P PAL+P+ F
Sbjct: 1 MAVDYVYDKTKLTDDEITRLKKLRDRNSEYWKEETYHIKSNNRVYPNIPALFPKHFPDPF 60

Query: 95 ENINNSKKISFYDQYETEGYLVGFARGLGVAKRNGDTEEQIRKYFKECFNSNTKIRDYST 154
ENINNSK+ISFYD+EYTE YLVGFA+GLGVAKRNG+TE+ IR+YFKEC N+ D T
Sbjct: 61 ENINNSKRISFYDKEYTEDYLVGFAQGLGVAKRNGETEKPIRQYFKECLNTGKYSDD--T 118

Query: 155 CQAEKFGSHPLIVKSHIFSLGPKIKNSHINSEILSVGNYTEWANQVIHHIENYVSFAAHL 214
C++++ S P V+S IF+L KIKNSHINSEILSVGNY EW ++ + S HL
Sbjct: 119 CKSQQ--SIPT-VRSDIFALNTKIKNSHINSEILSVGNYIEWLRPTLNQLS---SSQEHL 172

Query: 215 YSGLDPFHYIEVTDNSHVIGQTISLDEFRLNSLWEPWDSNVGKLKTTNADIRFNTKSE 274
YS +DPFHYIEVTDNSHVIGQTISLDEFRLNSLWEPWDS+VG+LKTTNADIRFNTKSE
Sbjct: 173 YSDVDPFHYIEVTDNSHVIGQTISLDEFRLNSLWEPWDSVVGELKTTNADIRFNTKSE 232

Query: 275 SLLVKEDYAGGARFRFAYDPKEA--KNTALIFEKNVTGTSDIIFENPIDDLKSLDGHQII 332
SLLVKEDYAGGARFRFAY K+ + L FEKN+TGTSDIIFENPIDDLKSLDGHQII
Sbjct: 233 SLLVKEDYAGGARFRFAYGLKDKVPETPVLTFEKNITGTSDIIFENPIDDLKSLDGHQII 292

Query: 333 KVNGTADKHAFRLSGKHQKGIYTLSQLQORPEGFLPKCKNAMIWRFMHNRLKPPIPYCALR 392
KVNGTADKHAFRLSGKHQKGIYTLSQLQORPEGF K + + + ALR
Sbjct: 293 KVNGTADKHAFRLSGKHQKGIYTLSQLQORPEGFFTKVQERDDISIYAQQAQAANTLFLALR 352

Query: 393 LNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVLGGEVFTWQNESNQ 452
LN+KNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVE RKGVLGGEVFTWQNESNQ
Sbjct: 353 LNDKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVESNRKGVLGGEVFTWQNESNQ 412

Query: 453 LSIGLMGGQAEQRSTFHNPDNDLTGTVKGFAGVYATWHQLQDKQTGAYADSWMQYQR 512
LS+GLM GQAEQRSTF NPDTDNDLTGTVKGFAG+YATWHQLQDKQTGAYADSW+QYQR
Sbjct: 413 LSVGLMSGQAEQRSTFRNPDTDNDLTGTVKGFAGIYATWHQLQDKQTGAYADSWVQYQR 472

Query: 513 FRHRINTEDGTERFTSKGITASIEAGYNALLAEHFTKKGNLSRVYLQPQAQLTYLGVNGK 572
FRHRINTED TERFTSKGITASIEAGYNALLAEHFTKKGN +R YLQPQAQLTYLGVNGK
Sbjct: 473 FRHRINTEDATERFTSKGITASIEAGYNALLAEHFTKKGNRVRYLQPQAQLTYLGVNGK 532

Query: 573 FSDSENAHVNLLGSRQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGER 632
FSDSENAHVNLLGSRQLQ+RVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGER
Sbjct: 533 FSDSENAHVNLLGSRQLQSRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGER 592

Query: 633 RVINNKAIAESQLGVAVKIKSHLTLQATFNROTGKHHQAKQGALNLQWTF 682
R+INNKAIAESQLGVAVKIKSHLTLQATFNROTGKHHQAKQGALNLQWTF
Sbjct: 593 RMINNKAIAESQLGVAVKIKSHLTLQATFNROTGKHHQAKQGALNLQWTF 642

tr Q6Q509 Lav (Fragment) [Haemophilus influenzae]

695 AA

align

Score = 962 bits (2486), Expect = 0.0

Identities = 494/665 (74%), Positives = 547/665 (81%), Gaps = 13/665 (1%)

```

Query: 23  IVSLFFSILYTSPLLAV-DYVYDKTKLTNDEITRLKKLRDKTSEYWKKETYLTITEDNPKV 81
      I+SLFFSILYTSPLLAV DY YD +KLTN++I RLKKLRD+ SEYWKKETYL+
Sbjct: 39  IISLFFSILYTSPLLAVDVTYDNSKLTNEQIERLKKLRDRNSEYWKKETYLLKSPPSNF 98

Query: 82  PPPPALYPR--TYQFENINNSKKISFYDQYETEGYLVGFARGLGVAKRNGDTEEQIRKYF 139
      P P L+P+ + FENI+NSK ISFYDQ+YTE YLVGFA+G GVAKRNGDTEE +RKYF
Sbjct: 99  PDIPVLFPKDSSVPFENIDNSKAISFYDQKYTEDYLVGFAQGFGVAKRNGDTEEPVRKYF 158

Query: 140  KECFNSNTKIRDYSTCQAEKFGSHPLIVKSHIFSLGPKIKNSHINSEILSVGNYTEWANQ 199
      KEC N+ D C+A S + +KS IF+ P IKNSHINSEIL+VGNYTE
Sbjct: 159  KECLNTGNYNND--NCKANPLASS-VSIKSDIFTPRPTIKNSHINSEILAVGNYTEL--- 212

Query: 200  VIHHIENYVSFAAHLYSGLDPFHYIEVTDNSHVIGQTISLDEFRLNSLWEPRWDSNVGK 259
      ++ + S+A HLYS DP + V DNSHVIGQTI L +L NSLWEPRW+SN+
Sbjct: 213  MLAAQPSASSWAHLYS--DPGLSLTVQDNSHVIGQTIDLGFLQLTNSLWEPRWNSNIDY 270

Query: 260  LKTTNADIRFNTKSESLLVKEDYAGGARFRFAYDPKEA--KNTALIFEKNVTGTSDIIFE 317
      L T NA+IRFNTK+ESLLV+ YAGGARFRFAYD K+ + L FE+N+TGTSIDIIFE
Sbjct: 271  LVTENAEIRFNTKNESLLVEGYAYAGGARFRFAYDLKDKAPETPVLTFEQNITGTSDIIFE 330

Query: 318  NPIDDLKSLDGHQIIKVNGTADKHAFLRSGKHQKGIYTLSSLQQRPEGFLPKCKNAMIWRF 377
      NPIDDLKSLDGHQI+KVNGTADK+AFRLSGK++KGIYTLSSLQQR EGF K +
Sbjct: 331  NPIDDLKSLDGHQIVKVNGTADKNAFLRSGKYRKGIYTLSSLQQRLEGFFTKLQERDDIAI 390

Query: 378  MHNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGV 437
      + + ALRLN+KNSDIFDRTLPRKGLWLRVIDGHS+QWVQGKTAP+EGYRKGV
Sbjct: 391  YAQQAQAANTLFALRLNDKNSDIFDRTLPRKGLWLRVIDGHSSQWVQGKTAPLEGYRKGV 450

Query: 438  QLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDNDNLTTGNVKGFGAGVYATWHQLQD 497
      QLGGEVFTWQNESNQ S+GLMGGQAEQRSTF NPDTDNLTTGN+KG GAGVYATWHQLQD
Sbjct: 451  QLGGEVFTWQNESNQFSVGLMGGQAEQRSTFRNPDTDNLTTGNMKGLGAGVYATWHQLQD 510

Query: 498  KQTGAYADSWMQYQFRHRINTEDGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVY 557
      KQTGAY DSW QYQFRHRINTEDGTERFTSKGITASIEAGYNALLAEH T KG +R Y
Sbjct: 511  KQTGAYVDSWAQYQFRHRINTEDGTERFTSKGITASIEAGYNALLAEHLTGKGTQIRFY 570

Query: 558  LQPQAQLTYLGVNGKFSDSENAHVNLLGSRQLQTRVGVAQAQFSLYKNIAIEPFPAAVNA 617
      LQPQAQLTYLGVNGKFSDSEN+ VNLLGSRQLQ+RVGVQAKAQF L KNI I+PFAAVN
Sbjct: 571  LQPQAQLTYLGVNGKFSDSSENSQVNLLGSRQLQSRVGVAQAQFLLNKNIVIQPFAAVNT 630

Query: 618  LYHNKPFGEVMDGERRVINNKTAIESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALN 677
      LYH+KPFGEV+DGERRVINNKTAIESQ G+AVKIKSHLTLQATFNRQTGKHH AKQGALN
Sbjct: 631  LYHSPKPFGEIDGERRVINNKTAIESQFGIAVKIKSHLTLQATFNRQTGKHHHAKQGALN 690

Query: 678  LQWTF 682
      LQWTF
Sbjct: 691  LQWTF 695

```

tr Q93N95 Lav (Fragment) [lav] [Haemophilus influenzae] 692 AA
align

Score = 954 bits (2467), Expect = 0.0

Identities = 487/664 (73%), Positives = 543/664 (81%), Gaps = 13/664 (1%)

```

Query: 23  IVSLFFSILYTSPLLAVDYVYDKTKLTND EITRLKKLRD KTSEYWK KETYLIT EDNPKVP 82
          I+SL S LY+SPLLAVDYVYDKTKLT+DEITRLKKLRD+ SEYWK+ETY I P
Sbjct: 38  ILSLLVSALYSSPLLAVDYVYDKTKLTDD EITRLKKLRDRDSEYWK EETYFIKSTPQSP 97

Query: 83  PFPALYPRTY--QFENINNSKISFYDQEYTEGYLVGFARGLGVAKRNGDTEEQIRKYFK 140
          P L+P+ FENINNSK+ISFYD+E+TE YLVGFA+G GVAKRNG+TEE +R+YFK
Sbjct: 98  NIPRLFPKNSFDSFENINNSKEISFYDKEFTEDYLVGFAQGFGVAKRNGETEETVRQYFK 157

Query: 141 ECFNSNTKIRDYSTCQAEKFGSHPLIVKSHIFSLGPKIKNSHINSEILSVGNYTEWANQV 200
          EC N+ D TC++ + + +KS IF+L +KNSHINSEIL+VGNYT+
Sbjct: 158 ECLNTGKHSND-PTCKS--YSTDAYNIKSDIFALNTIVKNSHINSEILAVGNYTKMLSA 214

Query: 201 IHHIENYVSFAAHLYSGLDPFHYIEVTDNSHVIGQTISLDEFRLNSLWEPRWDSNVGKL 260
          H ++A HLYS + + V DNSHVIGQTI L L NSLWEPRW+SN+ L
Sbjct: 215 QHSS----TWAEHLYSNAELS--LTVQDNSHVIGQTIDLGALILTNSLWEPRWNSNIDYL 268

Query: 261 KTTNADIRFNTKSESLLVKEDYAGGARFRFAYD--PKEAKNTALIFEKNVTGTSDIIFEN 318
          T NADIRFNTKSESLLVK +YAGGARFRFAYD K + L FE+N+TGTSDIIFEN
Sbjct: 269 ATENADIRFNTKSESLLVKGN YAGGARFRFAYDLQDKAPETPVLTFEQNITGTSDIIFEN 328

Query: 319 PIDDLKSLDGHQIIKVNGTADKHAFLRLSGKHQKGIYTLSSLQRRPEGFLPKCKNAMIWRFM 378
          PID+LKS L DGHQI+KVNGTADK+AFRLSGK++KGIYTLSSLQ+RPEGF K +
Sbjct: 329 PIDNLKSLDGHQIVKVNGTADKNAFLRLSGKYRKGIYTLSSLQRRPEGFFTKVQERDNIAIY 388

Query: 379 HNRLKPPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVQ 438
          + + ALRLN+KNSDIFDRTLPRKGLWLRVIDGHS+QWVQGKTAP+EGYRKGVQ
Sbjct: 389 AQQAQAANTLFALRLNDKNSDIFDRTLPRKGLWLRVIDGHSSQWVQGKTAPLEGYRKGVQ 448

Query: 439 LGGEVFTWQNESNQLSIGLMGGQAEQQRSTFHNPD TDNLTTGNVKGFGAGVYATWHQLQDK 498
          LGGEVFTWQNESNQ S+GLMGGQAEQQRSTF NPDTDNLTTGN+KGFGAGVYATWHQLQDK
Sbjct: 449 LGGEVFTWQNESNQFSVGLMGGQAEQQRSTFRNPDTDNLTTGNMKGFGAGVYATWHQLQDK 508

Query: 499 QTGAYADSWMQYQRFRRHINTEDGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYL 558
          QTGAY DSW+QYQRFRRH INTEDGTERFTSKGITASIEAGYNALLAEH T KG +R YL
Sbjct: 509 QTGAYIDSWVQYQRFRRHINTEDGTERFTSKGITASIEAGYNALLAEHVTGKGTQIRFYL 568

Query: 559 QPQAQLTYLGVNGKFSDSENHAVNLLGSRQLQTRVG VQAKAQFSLYKNIAIEPFPAAVNAL 618
          QPQAQLTYLGVNGKFSDSEN+ VNLLG RQLQ+RVGVQAKAQF L KNI I+PFAAVN L
Sbjct: 569 QPQAQLTYLGVNGKFSDSENSQVNLLGPRQLQSRVG VQAKAQFLLNKNIVIQPFAAVNTL 628

Query: 619 YHNKPFGEVMDGERRVINNKTAIESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNL 678
          YH+KPFGEV+DGERRVINNKTAIESQ G+AVKIKSHLTLQATFNRQTGK H AKQGALNL
Sbjct: 629 YHSPKPFGEIDGERRVINNKTAIESQFGI AVKIKSHLTLQATFNRQTGKRHHAKQGALNL 688

Query: 679 QWTF 682
          QWTF
Sbjct: 689 QWTF 692

```

tr Q93N94 Las (Fragment) [las] [Haemophilus influenzae biotype aegyptius]

703
AA
align

Score = 663 bits (1710), Expect = 0.0

Identities = 337/480 (70%), Positives = 386/480 (80%), Gaps = 5/480 (1%)

```
Query: 204 IENYVSFAAHLYSGLDPFHYIEVTDNSHVIGQTISLDEFRLNSLWEPRWDSNVGKLKTT 263
      I+NY S      GL      + V + S V G T+ L + L++SLWEPR++S+V L+T
Sbjct: 228 IDNYRSKFPDETRGLT----LTVKNQSEVRGATLQLLKMVLQDSLWEPRFNSDVHHLETQ 283

Query: 264 NADIRFNTKSESLLVKEDYAG-GARFRFAYDPKEAKNTALIFEKNVTGTSDIIFENPIDD 322
      NA+IRFN+ + L V E+Y G G+RF ++PKEA L F+K+VTGTS+I+FE PIDD
Sbjct: 284 NANIRFNSTNTRLTVHENYQGDGSRFFIKFNPKEATQPVLTFDKDVGTGTSNIVFEKPIDD 343

Query: 323 LKSLDGHQIIKVNGTADKHAFLRLSGKHQKGIYTLSSLQQRPEGFLPKCKNAMIWRFMHNRL 382
      LKSLDGHQIIKVNGTADKHAFLRLSGKHQKGIYTLSSLQQRPEGF K + +
Sbjct: 344 LKSLDGHQIIKVNGTADKHAFLRLSGKHQKGIYTLSSLQQRPEGFFTKVQERDDIAIYAQQA 403

Query: 383 KPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVLGGGE 442
      + ALRLN+KNSDIFDRTLPRKGLWLR+I GH +Q VQGKTAPVEG RKG+QLGG+
Sbjct: 404 QAANTLFAFLRLNDKNSDIFDRTLPRKGLWLRLLISGHLSQDVQGKTAPVEGNRKGILQGGD 463

Query: 443 VFTWQNESNQLSIGLMGGQAEQQRSTFHNPDNDNLTTGNVKGFGAGVYATWHQLQDKQTGA 502
      VF+ QN+ QLS GLMGGQAEQQRSTF N DTDNLTTG++KGFGAG+YATWHQLQDKQTGA
Sbjct: 464 VFSLQNQDYQLSFGLMGGQAEQQRSTFRNSDNDNLTTGSMKGFGAGIYATWHQLQDKQTGA 523

Query: 503 YADSWMQYQRFHRHINTEDGTERFTSKGITASIEAGYNALLAEHFTHKGNLSRVYLQPQA 562
      Y DSW+YQYQRFHRHINTEDG ERFTSKGITASIEAGYNALLAEH T+KG +R YLQPQA
Sbjct: 524 YVDSWVQYQRFHRHINTEDGIERFTSKGITASIEAGYNALLAEHLTEKGTQIRFYLPQA 583

Query: 563 QLTYLGVNGKFSSENHVNLLGSRQLQTRVGVAQAKAQFSLYKNIAIEPFAAVNALYHNK 622
      QLTYLGVNG +DS N+ VNLLGSRQLQ+RVG QAKAQF+ + +PF A+N++Y K
Sbjct: 584 QLTYLGVNGDLTDSGNSKVNLLGSRQLQSRVGAQAKAQFTFTNGVIFQPFVALNSIYQQK 643

Query: 623 PFGVEMDGERRVINNKTAIESQLGVAVKIKSHLTLOATFNROTGKHHQAKQGALNLQWTF 682
      PFGVE+D ERRVINNKTAIESQLGVA+KIKSHLTLOATFNROTGKHH AKQGALNLQWTF
Sbjct: 644 PFGVEIDNERRVINNKTAIESQLGVALKIKSHLTLOATFNROTGKHHHAKQGALNLQWTF 703
```

tr Q9JPL5 Autotransporter A [autA] [Neisseria meningitidis] 619 AA
align

Score = 389 bits (1000), Expect = e-107

Identities = 207/471 (43%), Positives = 302/471 (63%), Gaps = 24/471 (5%)

```
Query: 223 YIEVTDNSHVIGQTISLDEFRLNSLWEPRWDSNVGKLKTT-NADIRFNTKSESLLVKED 281
      ++++ + SHV GQ + L + L++SLWEPR S++ L+T+ NA IR NTK E L V +D
Sbjct: 162 HVKIENKSHVAGQVLELTGMTLTKDSLWEPRRHSIDIHTLETSDNARIRLNTKDEKLTVHKD 221

Query: 282 YAGGARFRFAYDPKEAKNTALIFEKNVTGTSDIIFENPIDDLKSLDGHQIIKVNGTADKH 341
      YAGGA F F YD +E+ AL FE V+G S ++ E ++LK+LDG ++I TAD
Sbjct: 222 YAGGADFLFGYDVRESDEPALTFEDKVSGQSGVVLERRPENLKTLDGRKLIAAK-TADSG 280

Query: 342 AFRLSGKHQKGIYTLSSLQQRPEGF-----LPKCKNAMIWR--FMHNRLKPPIPYCAL 391
      + +++G+Y L L+Q GF +P+ + + + + N L L
Sbjct: 281 SLAFKQNYRQGLYELLKQCEGGFCLGVQRLAIPAEAVLYAQQAAYAANTL-----FGL 334

Query: 392 RLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVLGGGEVFTWQNESN 451
      R ++ D++ R+ LWLR I G S+Q ++G A +G+RKGVQ+GGEVF QNE +
Sbjct: 335 RAADRGGDVYAADPSRQKLWLRFIGGRSHQNIRGGAA-ADGWRKGVQIGGEVFVRQNEGS 393
```

Query: 452 QLSIGLMGGQAEQRSTFHNPDNDLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQ 511
+L+IG+MGG+A Q ++ + ++ G+G GVYA WHQL+DKQTGAY D W+QYQ
Sbjct: 394 RLAIGVMGGRAGQHASVNGKG--GAAGSDLYGYGGGVYAAWHQLRDKQTGAYLDGWLQYQ 451

Query: 512 RFRHRINTEDGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNG 571
RF+HRIN E+ ER+ +KG TAS+E GYNAL+AE KGN++R YLQPQAQ TYLGVNG
Sbjct: 452 RFKHRINDENRAERYKTKGWTASVEGGYNALVAEGIVGKGNVRFYLPQAQFTYLGVNG 511

Query: 572 KFSDSENAHVNLLGSRQLQTRVGVOAKAQFSLYKNIAIEPFPAVNALYHNKPFGEVMDGE 631
F+DSE V LLGS Q Q+R G++AK +F+L + ++PFAA N L+ +K FGVEVMDGE
Sbjct: 512 GFTDSEGTAVGLLGSQWQSRAGIRAKTRFALRNGVNLQPFAAFNVLRHSKSFGEVMDGE 571

Query: 632 RRVINNKTALIESQLGVAVKIKSHLTLQATFNROTGKHHQAKQALNLQWTF 682
++ + +TA+E + G+ K H++ + + ++T K+ AL+L+W F
Sbjct: 572 KQTLAGRTALEGRFGIEAGWKGHMSARIGYGKRTDGD---KEAALSLKWL 619

tr Q9ZF58 Virulence-associated protein VapA [vapA] [Neisseria
meningitidis]

619
AA
align

Score = 388 bits (997), Expect = e-106

Identities = 224/576 (38%), Positives = 338/576 (57%), Gaps = 46/576 (7%)

Query: 130 DTEEQIRKYFKECFNSNTK-----IRDYSTCQAEKFGSHPLIVK-SHIFSLGPKI---- 178
D ++KY + + N K ++D + E + + + ++I LGPK
Sbjct: 67 DNMPVVKKYITDTYGDNLKDAVKKQLQDLYKTRPEAWENKKRTEEAYIEQLGPKFSILK 126

Query: 179 -KNSHINSEILSVGNYTEWANQVIHHIENYVSFAAHLYSGLDPFHYIEVTDNSHVIGQTI 237
KN + ++++ T +N + N + H +++ + SHV GQ +
Sbjct: 127 QKNPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLH-----VKIENKSHVAGQVL 176

Query: 238 SLDEFRLNSLWEPWRDSNVGKLT--NADIRFNTKSESLLVKEDYAGGARFRFAYDPKE 296
L + L++SLWEPR S++ L+T+ NA IR NTK E L V + Y GGA F F YD +E
Sbjct: 177 ELTKMTLKDSLWEPRRHSDIHTLETSDNARIRLNTKDEKLTVHKAYQGGADFLFGYDVRE 236

Query: 297 AKNTALIFEKNVTGTSDIIFENPIDDLKSLDGHQIIKVNGTADKHAFLSGKHQKGIYTL 356
+ AL FE+NV+G S+++ E ++LK+LDG ++I AD. ++F +++G+Y L
Sbjct: 237 SDEPALTFEQNVSGKSNVLERPENLKTLDGRKLIAAE-KADPNSFAFKQNYRQGLYEL 295

Query: 357 SLQQRPEGF-----LPKCKNAMIWR--FMHNRLKPPIPYCALRLNNKNSDIFDRTL 406
L+Q GF +P+ + + + N L LR ++ D++
Sbjct: 296 LLKQCEGGFCLGVQRLAIPAEAVLYAQQAANTL-----FGLRAADRGGDVYAADPS 349

Query: 407 RKGLWLRVIDGHSNQWVQGTAPVEGYRKGVLGGEVFTWQNESNQLSIGLMGGQAEQRS 466
R+ LWLR I G S+Q ++G A +G RKGVL+GGEVF QNE ++L+IG+MGG+A Q +
Sbjct: 350 RQKLWLRFIGGRSHQNIIRGGAA-ADGRRKGVQIGGEVFVRQNEGSRLAIGVMGGRAGQHA 408

Query: 467 TFHNPDNDLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFHRINTEDGTERF 526
+ + + G+G GVYA WHQL+DKQTGAY D W+QYQRF+HRIN E+ ER+
Sbjct: 409 SVNGKG--GAAGSYLHGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRVERY 466

Query: 527 TSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDSENAHVNLLGS 586
+KG TAS+E GYNAL+AE KGN++R YLQPQAQ TYLGVNG F+DSE V LLGS
Sbjct: 467 KTKGWTASVEGGYNALVAEGVVGKGNVRFYLPQAQFTYLGVNGGFTDSEGTAVGLLGS 526

Query: 587 RQLQTRVGQAKAQFSLYKNIAIEPFAAVNALYHNKPFVEMDGERRVINNKTAIESQLG 646
 Q Q+R G++AK +F+L + ++PFAA N L+ +K FGVEMDGE++ + +TA+E + G
 Sbjct: 527 GQWQSRAGIRAKTRFALRNGVNLQPFAAFNVLHRSKSFVEMDGEKQTLAGRTALEGRFG 586

Query: 647 VAVKIKSHLTQLQATFNRTGKHHQAKQGALNLQWTF 682
 + K H+ + + ++T K+ AL+L+W F
 Sbjct: 587 IEAGWKGHMFARIGYGKRTDGD---KEAALSLKWLF 619

tr Q9JSR2 Putative virulence associated protein [vapA] 619 AA
 [Neisseria align
 meningitidis (serogroup A)]

Score = 387 bits (993), Expect = e-106
 Identities = 223/576 (38%), Positives = 337/576 (57%), Gaps = 46/576 (7%)

Query: 130 DTEEQIRKYFKECFNSNTK-----IRDYSTCQAEKFGSHPLIVK-SHIFSLGPKI---- 178
 D ++KY + + N K ++D + E + + + ++I LGPK
 Sbjct: 67 DNMPVVVKYITDITYGDNLDKDAVKKQLQDLYKTRPEAWENKKRTEEAYIEQLGPKFSILK 126

Query: 179 -KNSHINSEILSVGNYTEWANQVIHHIENYVSFAAHLYSGLDPFHYIEVTDNSHVIGQTI 237
 KN + ++++ T +N + N + H +++ + SHV GQ +
 Sbjct: 127 QKNPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLH-----VKIENKSHVAGQVL 176

Query: 238 SLDEFRLNSLWEPWDSNVGKLT--NADIRFNTKSESLLVKEDYAGGARFRFAYDPKE 296
 L + L++SLWEPR S++ L+T+ NA IR NTK E L V + Y GGA F F YD +E
 Sbjct: 177 ELTKMTLKDSLWEPRRHSDIHMLETSNARIRLNTKDEKLTVHKAYQGGADFLFGYDVRE 236

Query: 297 AKNTALIFEKNVTGTSDIIFENPIDDLKSLDGHQIIKVNGTADKHAFLSGKHQKGIYTL 356
 + AL FE+ V+G S ++ E ++LK+LDG ++I AD ++F +++G+Y L
 Sbjct: 237 SDKPALTFEEKVSGQSGVVLERRPENLKTLDGRKLIAAE-KADSNSFAFKQNYRQGLYEL 295

Query: 357 SLQQRPEGF-----LPKCKNAMIWR--FMHNRLKPPIPYCALRLNNKNSDIFDRTL 406
 L+Q GF +P+ + + + + N L LR ++ D++
 Sbjct: 296 LLKQCEGGFCLGVQRLAIPAEAVLYAQYAAANTL-----FGLRAADRGDDVYAADPS 349

Query: 407 RKGLWLRVIDGHSNQWVQKTAPEGYRKGVLGGEVFTWQNESNQLSIGLMGGQAEQRS 466
 R+ LWLR I G S+Q ++G A +G RKGVQ+GGEVF QNE ++L+IG+MGG+A Q +
 Sbjct: 350 RQKLWLRFIGGRSHQNIRGGAA-ADGRRKGVQIGGEVFRVQNEGSRLAIGVMGGRAGQHA 408

Query: 467 TFHNPDTDNLTGTVNGKFGAGVYATWHQLQDKQTGAYADSWMQYQRFHRINTEDGTERF 526
 + + + G+G GVYA WHQL+DKQTGAY D W+QYQRF+HRIN E+ ER+
 Sbjct: 409 SVNGKG--GAAGSYLHGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERY 466

Query: 527 TSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPPAQQLTYLGVNGKFSSENHVNLLGS 586
 +KG TAS+E GYNAL+AE KGN++R YLQPPAQ TYLGVNG F+DSE V LLGS
 Sbjct: 467 KTKGWTASVEGGYNALVAEGVVGKGNVRFYLQPPAQFTYLGVNGGFTDSEGTAVGLLS 526

Query: 587 RQLQTRVGQAKAQFSLYKNIAIEPFAAVNALYHNKPFVEMDGERRVINNKTAIESQLG 646
 Q Q+R G++AK +F+L + ++PFAA N L+ +K FGVEMDGE++ + +TA+E + G
 Sbjct: 527 GQWQSRAGIRAKTRFALRNGVNLQPFAAFNVLHRSKSFVEMDGEKQTLAGRTALEGRFG 586

Query: 647 VAVKIKSHLTQLQATFNRTGKHHQAKQGALNLQWTF 682
 + K H++ + + ++T K+ AL+L+W F
 Sbjct: 587 IEAGWKGHMSARIGYGKRTDGD---KEAALSLKWLF 619

tr Q6J5G0 Putative virulence-associated protein (Fragment) [Haemophilus 291 AA
influenzae]

align

Score = 219 bits (557), Expect = 2e-55

Identities = 136/291 (46%), Positives = 165/291 (55%), Gaps = 47/291 (16%)

Query: 235 QTISLDEFRLNSLWEPRWDSNVGKLKTTNADIRFNTKSESLLVKE----- 280
Q I L E LNSLWEPRWDS+V L N+ IRFNTK+ESL+V E

Sbjct: 1 QVIHLYELNLENSLWEPRWDS+VSYLSLYNSHIRFNTKNESLVVGENRIRPTPDNALETE 60

Query: 281 -----DYA-GGARFRFAYD--PKEAKNTALIFEKNVTGTS 312
DY G RFAYD +EA L + V G +

Sbjct: 61 KDFKSRFSNIGYHSSSKIISYNNRSRDYVLGYPSIRFAYDLSEREADKPVLTLSKSVRGKT 120

Query: 313 DIIFENP-IDDLKSLDGHQIIKVNGTADKHAFRLSGKHQKGIYTLSQLQRPEGFLPKCKN 371
I+FE +++LK+L Q+IK + AF L +++KG Y L LQQ P GF +

Sbjct: 121 AIVFEEKALNNLNLTNRQLIKTETDIEPDFAFFLLEYYKKGRYRLFQQCPNGFCIGVEK 180

Query: 372 AMIWRFM----HNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKT 427
I + + ALRLN+KNSDIFDRTLPRKGLWLR+I GH +Q VQGKT

Sbjct: 181 LAIPTHLVASQAQAANTLFALRLNDKNSDIFDRTLPRKGLWLRISGHLSQDVQGKT 240

Query: 428 APVEGYRKGVQLGGEVFTWQNESQLSIGLMGGQAEQRSTFHNPDNDLTT 478

APVEG RKG+QLGG+VF+ QN+ Q S GLMGGQAEQRSTF NPDT N+TT

Sbjct: 241 APVEGNRKGQIQLGGDVFSLQNDYQFSFGLMGGQAEQRSTFRNPDTGNVTT 291

tr Q8X6C1 Putative beta-barrel outer membrane protein [z0402] 1349
[Escherichia coli
O157:H7] AA
align

Score = 142 bits (359), Expect = 2e-32

Identities = 100/327 (30%), Positives = 156/327 (47%), Gaps = 31/327 (9%)

Query: 371 NAMIWRFMHNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQCK-TAP 429
N M +H RL N +D+ + +W+R GH N+W G

Sbjct: 1039 NTMFTRLHERLG-----NTYYTDMVTGEQKQTTMWMRHEGGH-NKWRDGGGQLK 1087

Query: 430 VEGYRKGVQLGGEVFTW-QNESQLSIGLMGGQAEQRSTFHNPDNDLTTGNVKGFGAGV 488

+ R +QLGG+V W QN S++ +G+M G S + T +V G+ G+

Sbjct: 1088 TQSNRYVLQLGGDVAQWSQNGSDRWHVGMAGYGNDSKTISSRTGYRAKASVNGYSTGL 1147

Query: 489 YATWHQLQDKQTGAYADSWMQYQFRHRLNTED-GTERFTSKGITASIEAGYNALLAEHF 547

YATW+ + + GAY DSW QY F + + +D +E + SKG TAS+EAGY LAE

Sbjct: 1148 YATWYADDESNGAYLDSWAQYSWFDNTVKGDLLQSESYKSGFTASLEAGYKHKLAEFN 1207

Query: 548 TKKGNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRVGVQA--KAQFSL- 603

+G Y+QPQAQ+T++GV K +S V+ G +QTR+GV+ K+ +

Sbjct: 1208 GSQGTRNEWYVQPQAQVTWMGVKADKHRESNGTLVHSNGDGNVQTRLGVKTWLKSHHKMD 1267

Query: 604 -YKNIAIEPFAAVNALYHNKPFVEM-----DGERRVINNKTAIESQLGVAVKIKSHL 655

K+ +PF VN L+++K F M DG R + KT +E QL + + ++

Sbjct: 1268 DGKSREFQPFVEVNWLNHNSKDFSTSMGVSVTQDGARNIAEIKTGVEGQLNANLNVWGNV 1327

Query: 656 TLQATFNROTGKHHQAKQGALNLQWTF 682

+Q + + + ++W F

Sbjct: 1328 GVQV-----ADRGYNDSAMVGIKWQF 1349

tr Q7AH89 **AidA-I adhesin-like protein [ECs0362] [Escherichia coli** 1327
0157:H7] AA
align

Score = 142 bits (359), Expect = 2e-32

Identities = 100/327 (30%), Positives = 156/327 (47%), Gaps = 31/327 (9%)

Query: 371 NAMIWRFMHNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGK-TAP 429
N M +H RL N +D+ + +W+R GH N+W G

Sbjct: 1017 NTMFTTRLHERLG-----NTYYTDMVTGEQKQTTMWMRHEGGH-NKWRDGSQGLK 1065

Query: 430 VEGYRKGVQLGGEVFTW-QNESNQLSIGLMGGQAEQRSTFHNPDNDLTTGNVKGFGAGV 488
+ R +QLGG+V W QN S++ +G+M G S + T +V G+ G+

Sbjct: 1066 TQSNRYVLQLGGDVAQWSQNGSDRWHVGMAGYGNSSDKTISSTRTGYRAKASVNGYSTGL 1125

Query: 489 YATWHQLQDKQTGAYADSWMQYQFRHRINTED-GTERFTSKGITASIEAGYNALLAEHF 547
YATW+ + + GAY DSW QY F + + +D +E + SKG TAS+EAGY LAE

Sbjct: 1126 YATWYADDESNGAYLDSWAQYSWFDNTVKGDDLQSESYKSKGFTASLEAGYKHKLAEFN 1185

Query: 548 TKKGNSLRVYLQPPAQLTYLGVNG-KFSDSENAHVNLLGSRQLQTRVGVQA--KAQFSL- 603
+G Y+QPQAQ+T++GV K +S V+ G +QTR+GV+ K+ +

Sbjct: 1186 GSQGTRNEWYVQPQAQVTWMGVKADKHRESNGTLVHSNGDGNVQTRLGVKTWLKSHHKMD 1245

Query: 604 -YKNIAIEPFAAVNALYHNKPFVEM-----DGERRVINNKTAIESQLGVAVKIKSHL 655
K+ +PF VN L+++K F M DG R + KT +E QL + + ++

Sbjct: 1246 DGKSREFQPFVEVNWLNHNSKDFSTSMGVSVTQDGARNIAEIKTGVEGQLNANLNVWGNV 1305

Query: 656 TLQATFNROTGKHHQAKQGALNLQWTF 682

+Q + + + ++W F

Sbjct: 1306 GVQV-----ADRGYNDSAMVGIKWQF 1327

tr Q6KCW6 **YapH homolog [yapH] [Escherichia coli]** 2001 AA
align

Score = 139 bits (351), Expect = 1e-31

Identities = 87/294 (29%), Positives = 145/294 (48%), Gaps = 10/294 (3%)

Query: 398 SDIFDRTLPRKGLWLRVIDGHSNQWVQGKTA-PVEGYRKGVQLGGEVFTWQNESNQLSIG 456
+D+F +W+R I GH N+W + + R VQLGG + W + ++L G

Sbjct: 1709 TDVFTGEKKATSMWMRHIGGH-NRWKDSSSQLNTQSNRYVVQLGGSIAQWTDGQDRLQQG 1767

Query: 457 LMGGQAEQRSTFHNPDNDLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQFRHR 516
+M G ++S+ + + + G + G+ G+Y TW Q GAY D+W+QY F +

Sbjct: 1768 IMAGYGNEKSSTTSSLSGYKSKGAINGYSTGLYGTWQQNDGNDNGAYVDTWIQYGFNFNT 1827

Query: 517 INTED-GTERFTSKGITASIEAGYNALLAEHF+TKKGNSLRVYLQPPAQLTYLGVN-GKFS 574
+N E E + S+G T S+EAGY E +G+ Y+QPQ+Q+T++ V + +

Sbjct: 1828 VNGEKLAAESWKS RGTGSVEAGYTFKAGEFTGSQGS HYDWYIQPQSQITWMNV RASEHT 1887

Query: 575 DSENAHV NLLGSRQLQTRVGV---QAKAQFS LYNIAIEPFAAVNALYHNKPF GVEMDG 630
+ V L G +Q+R+GV + K+ K EPF VN +++ + +GV+MD

Sbjct: 1888 EKNGTKVQLSGDGNIQSRLGVRTYLKGKSASDDNKAHQFEPFVEVNW IHNTRSWGVKMDN 1947

Query: 631 ERRVINNKTAI-ESQLGVA VKIKSHLT LQATFNRTG-KHHQAKQGALNLQWTF 682
+ T I E + GV K+ +L + Q G K + Q L +++ F

Sbjct: 1948 TALSQDGATNIAEVKTGVQGLSDNLNVWGNVGVQAGDKGYSDAQAMLGIKYIF 2001

tr Q8FFF9 **Hypothetical protein ydeU [ydeU] [Escherichia coli** 291 AA
06] align

Score = 137 bits (344), Expect = 9e-31

Identities = 85/282 (30%), Positives = 141/282 (49%), Gaps = 10/282 (3%)

Query: 410 LWLRVIDGHSNQWVQGKTA-PVEGYRKG VQLGGEVFTWQNESNQLSIGLMGGQAEQRSTF 468
+W+R I GH N+W + + R VQLGG + W + ++L G+M G ++S+

Sbjct: 11 MWMRHIGGH-NRWKDSSSQLNTQSNRYVVQLGGSIAQWTDGQDRLQQGIMAGYGNEKSST 69

Query: 469 HNPDTDNLTGTVKGFAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTED-GTERFT 527
+ + + G + G+ G+Y TW Q GAY D+W+QY F + +N E E +

Sbjct: 70 TSSLSGYKSKGAINGYSTGLYGTWQQNDGNDNGAYVDTWIQYGFNNTVNGEKLAAESWK 129

Query: 528 SKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVN-GKFSDSENAHV NLLGS 586
S+G T S+EAGY E +G+ Y+QPQ+Q+T++ V + ++ V L G

Sbjct: 130 SRGFTGSVEAGYTFKAGEFTGSQGS HYDWYIQPQSQITWMNV RASEHTEKNGTKVQLSGD 189

Query: 587 RQLQTRVGV----QAKAQFS LYNIAIEPFAAVNALYHNKPF GVEMDGERRVINNKTAI- 641
+Q+R+GV + K+ K EPF VN +++ + +GV+MD + T I

Sbjct: 190 GNIQSRLGVRTYLKGKSASDDNKAHQFEPFVEVNW IHNTRSWGVKMDNTALSQDGATNIA 249

Query: 642 ESQLGVA VKIKSHLT LQATFNRTG-KHHQAKQGALNLQWTF 682
E + GV K+ +L + Q G K + Q L +++ F

Sbjct: 250 EVKTGVQGLSDNLNVWGNVGVQAGDKGYSDAQAMLGIKYIF 291

tr Q7BCK4 **VirG [virG] [Shigella flexneri]** 1102 AA
align

Score = 134 bits (338), Expect = 4e-30

Identities = 88/297 (29%), Positives = 149/297 (49%), Gaps = 12/297 (4%)

Query: 398 SDIFDRT---LPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKG VQLGGEVF-TWQNESNQL 453
S I D T L +W+R + GH+ + + R Q+GG++ T + + L

Sbjct: 806 STIVDPTTGQLSETTMWIRTVGGHNEHNADRQLKTTANRMVYQIGGDILKTNFTDHDGL 865

Query: 454 SIGLMGGQAEQRSTFHNPDNDLTGTVKGFAGVYATWHQLQDKQTGAYADSWMQYQRF 513
+G+MG Q S HN T + G V G+ AG+Y++W Q + ++TG Y D+W+QY F

Sbjct: 866 HVGIMGAYGYQDSKTHNKYTSYSSRGTVSGYTAGLYSSWFQDEKERTGLYMDAWLQYSWF 925

Query: 514 RHRINTEDGT-ERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGK 572
+ + + T E+++SKGIT ++EAGY +YL PQ Q+T GV

Sbjct: 926 NNTVKGDGLTGEKYSSKGITGALEAGYIYPTIRWTAHNNIDNALYLN PQVQITRHGVKAN 985

Query: 573 -FSDSENAHVNLLGSRQLQTRVGVOAK--AQFSLYKNI--AIEPFAAVNALYHNKPFGVE 627
 + + V G +Q ++G++ +Q + K EPF VN + +K +GV
 Sbjct: 986 DYIEHNGTMVTSSGGNNIQA KLGLRTSLISQSCIDKETLRKFEPFLEVNWKSSKQYGV I 1045

Query: 628 MDG-ERRVINNKTAIESQLGVAVKIKSHLT LQATFNRQTGKH-HQAKQGALNLQWTF 682
 M+G I N+ IE + GV ++ +L++ ++Q G + ++ QG L +++TF
 Sbjct: 1046 MNGMSNHQIGNRNVIELKTGVGGRLADNLSIWGNVSQQLGNNSYRDTQGILGVKYTF 1102

tr Q99Q93 **IcsA (VirG), outer membrane protein exposed to the bacterial surface** 1102
 by a C-terminal autotransporter domain and involved in AA
 the movement of intracellular bacteria by binding to align
 N-WASP (Invasion protein) [icsA (virG)] [Shigella
 flexneri]

Score = 134 bits (338), Expect = 4e-30
 Identities = 88/297 (29%), Positives = 149/297 (49%), Gaps = 12/297 (4%)

Query: 398 SDIFDRT--LPRKGLWLRVIDGHSNQWVGKTA PVEGYRKG VQLGGEVF-TWQNESNQL 453
 S I D T L +W+R + GH+ + + R Q+GG++ T + + L
 Sbjct: 806 STIVDPTTGQLSETTMWIRTVG GHNEHN LADRQLKTTANRMVYQIGGDILKTNFTDHDGL 865

Query: 454 SIGLMGGQAEQRSTFHNPDTDNLT TGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRF 513
 +G+MG Q S HN T + G V G+ AG+Y++W Q + ++TG Y D+W+QY F
 Sbjct: 866 HVGIMGAYGYQDSKTHNKYTSYSSRGTVSGYTAGLYSSWFQDEKERTGLYMDAWLQYSWF 925

Query: 514 RHRINTEDGT-ERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGK 572
 + + + T E+++SKGIT ++EAGY +YL PQ Q+T GV
 Sbjct: 926 NNTVKGDGLTGEKYSSKGITGALEAGYIYPTIRWTAHNNIDNALYLN PQVQITRHGVKAN 985

Query: 573 -FSDSENAHVNLLGSRQLQTRVGVOAK--AQFSLYKNI--AIEPFAAVNALYHNKPFGVE 627
 + + V G +Q ++G++ +Q + K EPF VN + +K +GV
 Sbjct: 986 DYIEHNGTMVTSSGGNNIQA KLGLRTSLISQSCIDKETLRKFEPFLEVNWKSSKQYGV I 1045

Query: 628 MDG-ERRVINNKTAIESQLGVAVKIKSHLT LQATFNRQTGKH-HQAKQGALNLQWTF 682
 M+G I N+ IE + GV ++ +L++ ++Q G + ++ QG L +++TF
 Sbjct: 1046 MNGMSNHQIGNRNVIELKTGVGGRLADNLSIWGNVSQQLGNNSYRDTQGILGVKYTF 1102

tr Q52298 **Virulence-associated VirG [Plasmid pMYSH6000]** 1102 AA
 align

Score = 134 bits (338), Expect = 4e-30
 Identities = 88/297 (29%), Positives = 149/297 (49%), Gaps = 12/297 (4%)

Query: 398 SDIFDRT--LPRKGLWLRVIDGHSNQWVGKTA PVEGYRKG VQLGGEVF-TWQNESNQL 453
 S I D T L +W+R + GH+ + + R Q+GG++ T + + L
 Sbjct: 806 STIVDPTTGQLSETTMWIRTVG GHNEHN LADRQLKTTANRMVYQIGGDILKTNFTDHDGL 865

Query: 454 SIGLMGGQAEQRSTFHNPDTDNLT TGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRF 513
 +G+MG Q S HN T + G V G+ AG+Y++W Q + ++TG Y D+W+QY F
 Sbjct: 866 HVGIMGAYGYQDSKTHNKYTSYSSRGTVSGYTAGLYSSWFQDEKERTGLYMDAWLQYSWF 925

Query: 514 RHRINTEDGT-ERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGK 572
 + + + T E+++SKGIT ++EAGY +YL PQ Q+T GV
 Sbjct: 926 NNTVKGDGLTGEKYSSKGITGALEAGYIYPTIRWTAHNNIDNALYLNPPVQITRHGVKAN 985

Query: 573 -FSDSENAHVNLGSRQLQTRVGQAK--AQFSLYKNI--AIEPFAAVNALYHNKPFGVE 627
 + + V G +Q ++G++ +Q + K EPF VN + +K +GV
 Sbjct: 986 DYIEHNGTMVTSSGGNNIQAKLGLRTSLISQSCIDKETLRKFEPFLEVNWKWSSKQYGV 1045

Query: 628 MDG-ERRVINNKTAIESQLGVAVKIKSHLTLQATFNRQTGKH-HQAKQGALNLQWTF 682
 M+G I N+ IE + GV ++ +L++ ++Q G + ++ QG L +++TF
 Sbjct: 1046 MNGMSNHQIGNRVIELKTGVGGRLADNLSIWGNVSQQLGNNSYRDTQGILGVKYTF 1102

tr Q9JMS3 YchA protein [ychA] [Escherichia coli] 1371 AA
align

Score = 134 bits (337), Expect = 6e-30

Identities = 122/461 (26%), Positives = 193/461 (41%), Gaps = 46/461 (9%)

Query: 266 DIRFNTKSESLLVKEDYAGG---ARFRFAYDPKEAKNTALIFEKNVTGTSDIIFENPIDD 322
 D+R L + +Y G D + L+ + + +G + + N
 Sbjct: 913 DLRSAAPGNILTIGGNYTGNNGTLLINTVLDDSSSATDKLVIKGDASGKTRVAVTNVGGS 972

Query: 323 -LKSLDGHQIIKVNGTADKHAFRLSGKHQKGIYTLSSLQQRPEG-----FLPKCKNAMIWR 376
 +L+ ++I V+G A F +G+ G Y +L + P +L KN R
 Sbjct: 973 GANTLNSIEVIHVDGNAANAEFIQAGRIAAGAYDYTLGRGPGSNYGNWYLSSSKNTPEPR 1032

Query: 377 -----FMHNRLKPPPIPYCALRLNNKNSDIFDRTLPRKG-----LWL 412
 N L+P + N+ R R G +W+
 Sbjct: 1033 PDPEPTPEGHDNNLRPEASSYTANIAAANTMFVTRLHERLGQTQYVDAITGEPKATSMWM 1092

Query: 413 RVIDGHSNQWVQ GK-TAPVEGYRKGVLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFHN 470
 R GH N+W G + R +QLGG++ W +N+ +G+M G S+
 Sbjct: 1093 RHEGGH-NRWRDGSQGLKTQSNRYVIQLGGDIAQWDWGGTNRWHLGVMAGYGNNHSSSTGA 1151

Query: 471 PDTDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTEDGT--ERFTS 528
 T + G+V G+ G+YATW+ + GAY D+W QY F + + DG E + S
 Sbjct: 1152 VRTGYHSGKSVNGYSTGLYATWYADDETHNGAYLDTWAQYGWFDNHVK-GDGLPGESWKS 1210

Query: 529 KGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLGSR 587
 KG+TAS+E GY + E + GN Y+QPQAQL ++GV + +S + G
 Sbjct: 1211 KGLTASLETGYAWKIGEFSSNYGNLNEWYVQPQAQLVWMGVKADELYESNGTLIESTGDG 1270

Query: 588 QLQTRVGVA---KAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGERRVINNKTAI-E 642
 + TR+GV+ + K+ PF VN L++ + FGV M+GE + I E
 Sbjct: 1271 NVHTRLGVKTIKRLNKMDDGKSREFSPFVEVNLHNTRDFGVRMNGEPVYQDGTNRNIGE 1330

Query: 643 SQLGVAVKIKSHLTLQATFNRQTG-KHHQAKQGALNLQWTF 682
 + GV +I HL L Q G K + L +++TF
 Sbjct: 1331 VKTGVEGQINPHLNLWGNVRVQVGDKGYNDTSAMLGVKYTF 1371

tr Q6WE27 IcsA [icsA] [Shigella flexneri] 1102 AA
align

Score = 134 bits (336), Expect = 7e-30

Identities = 90/301 (29%), Positives = 150/301 (48%), Gaps = 20/301 (6%)

```

Query: 398  SDIFDRT---LPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVLGGGEVF-TWQNESNQL 453
           S I D T  L   +W+R + GH+   +   R   Q+GG++ T   + + L
Sbjct: 806  STIVDPTTGQLSETTMWIRTVGGHNEHNLADRQLKTTANRMVYQIGGDILKTNFTDHDGL 865

Query: 454  SIGLMGGQAEQRSTFHNPDNDLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRF 513
           +G+MG   Q S  HN  T   + G V G+ AG+Y++W Q + ++TG Y D+W+QY  F
Sbjct: 866  HVGIMGAYGYQDSKTHNKYTSYSSRGTVSGYTAGLYSSWFQDEKERTGLYMDAWLQYGWF 925

Query: 514  RHRINTEDGT-ERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGK 572
           + + + T E+++SKGIT ++EAGY           T           +YL PQ Q+T  GV
Sbjct: 926  NNTVKGDGLTGEKYSSKGITGALEAGYIYPTIRWTTNNIDNALYLNPPQVQITRHGVKAN 985

Query: 573  -FSDSENAHVNLLGSRQLQTRVGVAQAQFSLYKNIAI-----EPFAAVNALYHNKP 623
           + +   V   G   +Q ++G++   SL + I           EPF VN + +K
Sbjct: 986  DYIEHNGTMTSSGVNNIQAKLGLRT---SLISHSCIDKETLRKFEPFLEVNWKWSSKQ 1041

Query: 624  FGVEMDG-ERRVINNKTAIESQLGVAVKIKSHLTLQATFNRTGKH-HQAKQGALNLQWT 681
           +GV M+G   I N+  IE + GV  ++  +L++   ++Q G + ++  QG L +++T
Sbjct: 1042 YGVIMNGMSNHQIGNRNVIELKTGVGGRADNLSIWGNVSQQLGNNSYRDTQGILGVKYT 1101

Query: 682  F 682
           F
Sbjct: 1102 F 1102

```

tr Q8ZHA1 **Putative autotransporter protein [yapH] [Yersinia** 3705 AA
 pestis] align

Score = 130 bits (326), Expect = 1e-28

Identities = 106/385 (27%), Positives = 170/385 (43%), Gaps = 36/385 (9%)

```

Query: 324  KSLDGHQIIKVNGTADKHAFLRSGKHQKGIYTLQQRPEGFLPKCKNAMIWRFMHNRLK 383
           ++ +G +II V G +   F L+G+   G Y   L Q   P   N +   +R
Sbjct: 3331 RTFEGIKIIDVGDSAGQ-FTLNGRAVGGAYEYFLYQGGAS-TPDDGNWYLRTADDRRP 3388

Query: 384  PPIPYCALRLNNKN-----SDIFDRTLPRKGLWLRVIDGHSNQWVQGKTA 428
           P   Y A   N           +D+F           LWLR   H+
Sbjct: 3389 EPASYTANLAAANNMFVTSIADRMGETLYTDVFTGEQKTTSLWLRNEGSHNRSRDDSGEL 3448

Query: 429  PVEGYRKGVLGGGEVFTWQNESNQL-SIGLMGGQAEQRSTFHNPDNDLTTGNVKGFGAG 487
           + R +QLGG+V W   + L +G+M G A   S+           +TG+V G+ G
Sbjct: 3449 KTQDNRYVMQLGGDVAQWSRNAQDLWRVGMAGYANSSSSTVAQVAGYRSTGSDGYSVG 3508

Query: 488  VYATWHQLQDKQTGAYADSWMQYQRFHRINTED-GTERFTSKGITASIEAGYNALLAEH 546
           +Y +W           TGAY DSW+QY  F +R++ +D  TE++ SKG TAS+E GY   + E
Sbjct: 3509 IYGSWLADNADDTGAYVDSWVQYSWFDNRVSGQDLATEKYDSKGFTASVEGGYAFKVGES 3568

Query: 547  FTKKGNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLLGSRQLQTRVGVA-----KA 599
           +           ++QP+AQ+ ++GV   +++   ++  G+  +QTR+G +A   KA
Sbjct: 3569 VNQS-----YFIQPKAQVVMGVKADDHTETNGTVISGDGNGNIQTRLGAKAFINPSDKA 3623

Query: 600  QFSLYKNIAIEPFAAVNALYHNKPFGEVMDGER-RVINNKTAIESQLGVAVKIKSHLTLQ 658
           + S   A +PF   N +++ K FG  +DG   +           E +LGV  ++ S L L

```

Sbjct: 3624 KVS---GPAFKPFVEANWIHNTKDFGTTLDGVTVKQAGTANIAELKLGVDGQVNSQLNLW 3680

Query: 659 ATFNRQTG-KHHQAKQGALNLQWTF 682

+Q G K + L +++ F

Sbjct: 3681 GNIGQQVGNKGYSETSVVLGVKYNF 3705

tr Q8CZU2 Putative autotransporter adhesin [yapH] [Yersinia pestis] 3710 AA
align

Score = 130 bits (326), Expect = 1e-28

Identities = 106/385 (27%), Positives = 170/385 (43%), Gaps = 36/385 (9%)

Query: 324 KSLDGHQIIKVNGTADKHAFRLSGKHQKGIYTLSLQQRPEGFLPKCKNAMIWRFMHNRLK 383

++ +G +II V G + F L+G+ G Y L Q P N + +R

Sbjct: 3336 RTFEGIKIIDVGGSAGQ-FTLNGRAVGGAYEYFLYQGGAS-TPDDGNWYLRTTEADRRP 3393

Query: 384 PPIPYCALRLNNKN-----SDIFDRTLPRKGLWLRVIDGHSNQWVQGKTA 428

P Y A N +D+F LWLR H+

Sbjct: 3394 EPASYTANLAAANNMFVTS LADRMGETLYTDVFTGEQKTTSLWLRNEGSHNRSRDDSGEL 3453

Query: 429 PVEGYRKGVQLGGEVFTWQNESNQL-SIGLMGGQAEQRSTFHNPD'TDNL'TTGNVKGFGAG 487

+ R +QLGG+V W + L +G+M G A S+ +TG+V G+ G

Sbjct: 3454 KTQDNRYVMQLGGDVAQWSRNAQDLWRVGVMMAGYANSSSSTVAQVAGYRSTGSVDGYSVG 3513

Query: 488 VYATWHQLQDKQTGAYADSWMQYQRFRRHINTED-GTERFTSKGITASIEAGYNALLAEH 546

+Y +W TGAY DSW+QY F +R++ +D TE++ SKG TAS+E GY + E

Sbjct: 3514 IYGSWLADNADDTGAYVDSWVQYSWFDNRVSGQDLATEKYDSKGFTASVEGGYAFKVGES 3573

Query: 547 FTKKGNLSRLRVYLQPPAQLTYLGVNG-KFSDSENAHVNLLGSRQLQTRVGVQA-----KA 599

+ ++QP+AQ+ ++GV +++ ++ G+ +QTR+G +A KA

Sbjct: 3574 VNQS-----YFIQPKAQVVMGVKADDHTETNGTVISGDGNGNIQTRLGAKAFINPSDKA 3628

Query: 600 QFSLYKNIAIEPFAAVNALYHNKPFVEMDGER-RVINNKTAIESQLGVAVKIKSHLTLO 658

+ S A +PF N +++ K FG +DG + E +LGV ++ S L L

Sbjct: 3629 KVS---GPAFKPFVEANWIHNTKDFGTTLDGVTVKQAGTANIAELKLGVDGQVNSQLNLW 3685

Query: 659 ATFNRQTG-KHHQAKQGALNLQWTF 682

+Q G K + L +++ F

Sbjct: 3686 GNIGQQVGNKGYSETSVVLGVKYNF 3710

tr Q9F289 YapD protein [yapD] [Yersinia pestis] 1457 AA
align

Score = 130 bits (326), Expect = 1e-28

Identities = 106/385 (27%), Positives = 170/385 (43%), Gaps = 36/385 (9%)

Query: 324 KSLDGHQIIKVNGTADKHAFRLSGKHQKGIYTLSLQQRPEGFLPKCKNAMIWRFMHNRLK 383

++ +G +II V G + F L+G+ G Y L Q P N + +R

Sbjct: 1083 RTFEGIKIIDVGGSAGQ-FTLNGRAVGGAYEYFLYQGGAS-TPDDGNWYLRTTEADRRP 1140

Query: 384 PPIPYCALRLNNKN-----SDIFDRTLPRKGLWLRVIDGHSNQWVQGKTA 428

P Y A N +D+F LWLR H+

Sbjct: 1141 EPASYTANLAAANNMFVTS LADRMGETLYTDVFTGEQKTTSLWLRNEGSHNRSRDDSGEL 1200

Query: 429 PVEGYRKGVQLGGEVFTWQNESNQL-SIGLMGGQAEQRSTFHNPDNDNLTGNNVKGFGAG 487
+ R +QLGG+V W + L +G+M G A S+ +TG+V G+ G
Sbjct: 1201 KTQDNRYVMQLGGDVAQWSRNAQDLWRVGVGMAGYANSSSSTVAQVAGYRSTGSVDGYSVG 1260

Query: 488 VYATWHQLQDKQTGAYADSWMQYQFRHRINTED-GTERFTSKGITASIEAGYNALLAEH 546
+Y +W TGAY DSW+QY F +R++ +D TE++ SKG TAS+E GY + E
Sbjct: 1261 IYGSWLADNADDTGAYVDSWVQYSWFDNRVSGQDLATEKYDSKGFTASVEGGYAFKVGES 1320

Query: 547 FTKKGNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLLGSRQLQTRVGVQA-----KA 599
+ ++QP+AQ+ ++GV +++ ++ G+ +QTR+G +A KA
Sbjct: 1321 VNQS-----YFIQPKAQVVMGVKADDHTETNGTVISGDGNGNIQTRLGAKAFINPSDKA 1375

Query: 600 QFSLYKNIAIEPFAAVNALYHNKPFVEMDGER-RVINNKTAIESQLGVAVKIKSHLTLQ 658
+ S A +PF N +++ K FG +DG + E +LGV ++ S L L
Sbjct: 1376 KVS---GPAFKPFVEANWIHNTKDFGTTLDGVTVKQAGTANIAELKLGVDGQVNSQLNLW 1432

Query: 659 ATFNRQTG-KHHQAKQGALNLQWTF 682
+Q G K + L +++ F
Sbjct: 1433 GNIGQQVGNKGYSETSVVLGVKYNF 1457

tr Q9F285 YapH protein [yapH] [Yersinia pestis] 3705 AA
align

Score = 130 bits (326), Expect = 1e-28
Identities = 106/385 (27%), Positives = 170/385 (43%), Gaps = 36/385 (9%)

Query: 324 KSLDGHQIIKVGNTADKHAFLSGKHQKGIYTLSSLQQRPEGFLPKCKNAMIWRFMHNRLK 383
++ +G +II V G + F L+G+ G Y L Q P N + +R
Sbjct: 3331 RTFEGIKIIDVGDSAGQ-FTLNGRAVGGAYEYFLYQGGAS-TPDDGNWYLRTTEADRRP 3388

Query: 384 PPIPYCALRLNNKN-----SDIFDRTLPRKGLWLRVIDGHSNQWVQGKTA 428
P Y A N +D+F LWLR H+
Sbjct: 3389 EPASYTANLAAANNMFVTSALDRMGETLYTDVFTGEQKTTSLWLRNEGSHNRSRDDSGEL 3448

Query: 429 PVEGYRKGVQLGGEVFTWQNESNQL-SIGLMGGQAEQRSTFHNPDNDNLTGNNVKGFGAG 487
+ R +QLGG+V W + L +G+M G A S+ +TG+V G+ G
Sbjct: 3449 KTQDNRYVMQLGGDVAQWSRNAQDLWRVGVGMAGYANSSSSTVAQVAGYRSTGSVDGYSVG 3508

Query: 488 VYATWHQLQDKQTGAYADSWMQYQFRHRINTED-GTERFTSKGITASIEAGYNALLAEH 546
+Y +W TGAY DSW+QY F +R++ +D TE++ SKG TAS+E GY + E
Sbjct: 3509 IYGSWLADNADDTGAYVDSWVQYSWFDNRVSGQDLATEKYDSKGFTASVEGGYAFKVGES 3568

Query: 547 FTKKGNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLLGSRQLQTRVGVQA-----KA 599
+ ++QP+AQ+ ++GV +++ ++ G+ +QTR+G +A KA
Sbjct: 3569 VNQS-----YFIQPKAQVVMGVKADDHTETNGTVISGDGNGNIQTRLGAKAFINPSDKA 3623

Query: 600 QFSLYKNIAIEPFAAVNALYHNKPFVEMDGER-RVINNKTAIESQLGVAVKIKSHLTLQ 658
+ S A +PF N +++ K FG +DG + E +LGV ++ S L L
Sbjct: 3624 KVS---GPAFKPFVEANWIHNTKDFGTTLDGVTVKQAGTANIAELKLGVDGQVNSQLNLW 3680

Query: 659 ATFNRQTG-KHHQAKQGALNLQWTF 682
+Q G K + L +++ F
Sbjct: 3681 GNIGQQVGNKGYSETSVVLGVKYNF 3705

tr Q74QP7 **Putative autotransporter protein [yapH] [Yersinia pestis]** 3710 AA
align

Score = 130 bits (326), Expect = 1e-28

Identities = 106/385 (27%), Positives = 170/385 (43%), Gaps = 36/385 (9%)

Query: 324 KSLDGHQIIKVNGTADKHAFRLSGKHQKGIYTLQLQRPEGLPKCKNAMIWRFMHNRLK 383
++ +G +II V G + F L+G+ G Y L Q P N + +R
Sbjct: 3336 RTFEGIKIIDVGGDSAGQ-FTLNGRAVGGAYEYFLYQGGAS-TPDDGNWYLRTTEADRRP 3393

Query: 384 PPIPYCALRLNKN-----SDIFDRTLPRKGLWLRVIDGHSNQWVQGKTA 428
P Y A N +D+F LWLR H+
Sbjct: 3394 EPASYTANLAAANNMFVTSLADRMGETLYTDVFTGEQKTTSLWLRNEGSHNRSRDDSGEL 3453

Query: 429 PVEGYRKGVQLGGEVFTWQNESNQL-SIGLMGGQAEQRSTFHNPDNDLTGNNVKGFGAG 487
+ R +QLGG+V W + L +G+M G A S+ +TG+V G+ G
Sbjct: 3454 KTQDNRYVMQLGGDVAQWSRNAQDLWRVGMAGYANSSSSTVAQVAGYRSTGSDVDGYSVG 3513

Query: 488 VYATWHQLQDKQGTGAYADSWMQYQFRHRINTED-GTERFTSKGITASIEAGYNALLAEH 546
+Y +W TGAY DSW+QY F +R++ +D TE++ SKG TAS+E GY + E
Sbjct: 3514 IYGSWLADNADDTGAYVDSWVQYSWFDNRVSGQDLATEKYDSKGFTASVEGGYAFKVGES 3573

Query: 547 FTKKGNSLRVYLQPPAQLTYLGVNG-KFSDSENAHVNLLGSRQLQTRVGVQA-----KA 599
+ ++QP+AQ+ ++GV +++ ++ G+ +QTR+G +A KA
Sbjct: 3574 VNQS-----YFIQPKAQVVMGVKADDTETNGTVISGDGNGNIQTRLGAKAFINPSDKA 3628

Query: 600 QFSLYKNIAIEPFAAVNALYHNKPFGVEMDGER-RVINNKTAIESQLGVAVKIKSHLTLQ 658
+ S A +PF N +++ K FG +DG + E +LGV ++ S L L
Sbjct: 3629 KVS---GPAFKPFVEANWIHNTKDFGTTLDGVTVKQAGTANIAELKLGVDGQVNSQLNLW 3685

Query: 659 ATFNRTG-KHHQAKQGALNLQWTF 682
+Q G K + L +++ F
Sbjct: 3686 GNIGQQVGNKGYSETSVVLGVKYNF 3710

tr Q9F286 **YapG protein (Putative ATP-binding transport component)** 994
(Putative AA
autotransporter protein) [yapG] [Yersinia pestis] align

Score = 129 bits (324), Expect = 2e-28

Identities = 84/272 (30%), Positives = 132/272 (47%), Gaps = 12/272 (4%)

Query: 410 LWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTF 468
+W+ G S + ++G VQLGG++ W NE IG++ G + +
Sbjct: 723 MWMHTQGGRSQFGHTVEQLNIKGNYYSVQLGGDIAQWATNEQSGRIGMLAGLGKATNHS 782

Query: 469 HNPDTNDLTGNNVKGFGAGVYATWHQLQDKQGTGAYADSWMQYQFRHRINTED-GTERFT 527
H+ T + G V G+ G+YATW Q TG Y D+ QY F + +N +D E++
Sbjct: 783 HSKVTSYHSRGAVDGYNLGIYATWFADQQHNTGVYIDTLAQYSWFNNVNGQDKAEKYYK 842

Query: 528 SKGITASIEAGYNALLAEHFTKKGNSLRVYLQPPAQLTYLGVNGK-FSDSENAHVNLLGS 586
S G T SIE+GY LA + L ++QP AQ+T+ G+N + ++ A V+ +
Sbjct: 843 SSGFTTIESGYTFNLA-----NSDQLSYFIQPNQITWAGINAQTHKTADGAVVSYRNN 897

Query: 587 RQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGERRVINNK--TAIESQ 644

TR+G +A Q N PF AVN ++ N+ G + G+ I+NK + E
 Sbjct: 898 GHFITRIGAKAYLQTHDTLNTKFTPFVAVNWIHQNTGTTISGQG--IDNKIQNSTEFN 955
 Query: 645 LGVAVKIKSHLTLQATFNRQTGKHHQAKQGAL 676
 +GV +I L + A N Q G+++ AL
 Sbjct: 956 VGVESQIDQQLHIWANINHQIGRYNYTDTNAL 987

tr Q74RV9 Putative autotransporter protein [YP2907] [Yersinia pestis] 994 AA

align

Score = 129 bits (324), Expect = 2e-28

Identities = 84/272 (30%), Positives = 132/272 (47%), Gaps = 12/272 (4%)

Query: 410 LWLRVIDGHSNQWVQGKTAPVEGYRKGVLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTF 468
 +W+ G S + ++G VQLGG++ W NE IG++ G + +
 Sbjct: 723 MWMHTQGGRSQFGHTVEQLNIKNYYSVQLGGDIAQWATNEQSGRIGMLAGLGKATNHS 782
 Query: 469 HNPDTDNLTGTVKGFAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTED-GTERFT 527
 H+ T + G V G+ G+YATW Q TG Y D+ QY F + +N +D E++
 Sbjct: 783 HSKVTSYHSRGAVDGYNLGIYATWFADQQHNTGVYIDTLAQYSWFNNAVNGQDKAEKYYK 842
 Query: 528 SKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGK-FSDSENAHVNLLGS 586
 S G T SIE+GY LA + L ++QP AQ+T+ G+N + ++ A V+ +
 Sbjct: 843 SSGFTTSIESGYTFNLA-----NSDQLSYFIQPNQAQITWAGINAQTHKTADGAVVSYRNN 897
 Query: 587 RQLQTRVGQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGERRVINNK--TAIESQ 644
 TR+G +A Q N PF AVN ++ N+ G + G+ I+NK + E
 Sbjct: 898 GHFITRIGAKAYLQTHDTLNTKFTPFVAVNWIHQNTGTTISGQG--IDNKIQNSTEFN 955
 Query: 645 LGVAVKIKSHLTLQATFNRQTGKHHQAKQGAL 676
 +GV +I L + A N Q G+++ AL
 Sbjct: 956 VGVESQIDQQLHIWANINHQIGRYNYTDTNAL 987

sp P77286 Hypothetical protein ydeU [ydeU] [Escherichia 466 AA
YDEU_ECOLI coli] align

Score = 129 bits (323), Expect = 2e-28

Identities = 87/323 (26%), Positives = 155/323 (47%), Gaps = 23/323 (7%)

Query: 371 NAMIWRFMHNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPV 430
 N++ +H+RL P + +D +W+R + GH
 Sbjct: 156 NSLFSHRLHDLRGEP-----QYTDLSLHSQGSASSMWMRHVGGHERSRAGDQQLNT 205
 Query: 431 EGYRKGVLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFHNPDNDLTGTVKGFAGVY 489
 + R +QLGG++ W N ++ +G+M G A Q S + + G + G+ AG+Y
 Sbjct: 206 QANRYVLQLGGDLAQWSSNAQDRWHLGVMAGYANQHSNTQSNRVGYKSDGRISGYSAGLY 265
 Query: 490 ATWHQLQDKQTGAYADSWMQYQFRHRINTED-GTERFTSKGITASIEAGYNALLAEHFT 548
 ATW+Q +TGAY DSW Y F + +++++ + + S+G+TAS+E GY
 Sbjct: 266 ATWYQNDANKTGAYVDSWALYNWFDNSVSSDNRSADDYDSRGVTASVEGGYTFEAGTFSG 325
 Query: 549 KKGNSLRVYLQPQAQLTYLGV-NGKFSDSENAHVNLLGSRQLQTRVGQVQ----AKAQFSL 603

```

      +G      Y+QPQAQ+T++GV +   +   +   G   +QTR+GV+   +   Q
Sbjct: 326 SEGTLNTWYVQPQAQITWMGVKDSHDTRKDGTRIETEGDGNVQTRLGVKTYLNSHHQRDD 385

Query: 604 YKNIAIEPFAAVNALYHNKPFGEVMDGE---RRVINNKTAIESQLGVAVKIKSHLTLQAT 660
      K   +P+   N + ++K + V+M+G+   R   N   E + GV   K+ ++L+L
Sbjct: 386 GKQREFQPYIEANWINNSKVYAVKMNGQTVGREGARNLG--EVRTGVEAKVNNNLSLWGN 443

Query: 661 FNRQTG-KHHQAKQGALNLQWTF 682
      Q G K +   QG L +++++
Sbjct: 444 VGVQLGDKGYSDTQGMLGVKYSW 466

```

```

tr Q8XAY3 Putative ATP-binding component of a transport system and      466
          adhesin                                                         AA
          protein [z2196] [Escherichia coli O157:H7]                     align

```

Score = 129 bits (323), Expect = 2e-28

Identities = 86/321 (26%), Positives = 156/321 (47%), Gaps = 19/321 (5%)

```

Query: 371 NAMIWRFMHNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPV 430
      N++   +H+RL P   +L   + S               +W+R + GH
Sbjct: 156 NSLFSHRLHDLRGEPQYTDLSHSQDSASS-----MWMRHVGGHERSSAGDQQLNT 205

Query: 431 EGYRKGVLGGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFHNPDNDLTTGNVKGFGAGVY 489
      + R   +QLGG++ W N ++ +G+M G A Q S   +   + G + G+ AG+Y
Sbjct: 206 QANRYVLQLGGDLAQWSSNAQDRWHLGVMMAGYANQHSNTQSNRVGYKSDGRISGYSAGLY 265

Query: 490 ATWHQLQDKQTGAYADSWMQYQFRHRINTED-GTERFTSKGITASIEAGYNALLAEHFT 548
      ATW+Q   +TGAY DSW Y F + +++++   + + S+G+TAS+E GY
Sbjct: 266 ATWYQNDANKTGAYVDSWALYNWFDNSVSSDNRSADDYDSRGVTASVEGGYTFEAGTCSG 325

Query: 549 KKGNSLRVYLQPQAQLTYLGV-NGKFSDSENAHVNLGSRQLQTRVGVO----AKAQFSL 603
      +G      Y+QPQAQ+T++GV +   +   +   G   +QTR+GV+   +   Q
Sbjct: 326 SEGTLNTWYVQPQAQITWMGVKDSHDHARKDGTRIETEGDGNVQTRLGVKTYLNSHHQRDD 385

Query: 604 YKNIAIEPFAAVNALYHNKPFGEVMDGERRVINNKTAI-ESQLGVAVKIKSHLTLQATFN 662
      K   +P+   N + ++K + V+M+G+   +   + E + GV   K+ ++L+L
Sbjct: 386 GKQREFQPYIEANWINNSKVYAVKMNGQTVSRDGARNLGEVVRTGVEAKVNNNLSLWGNVG 445

Query: 663 RQTG-KHHQAKQGALNLQWTF 682
      Q G K +   QG L +++++
Sbjct: 446 VQLGDKGYSDTQGMLGVKYSW 466

```

```

tr Q7AE01 Putative ATP-binding component of a transport system and      466
          adhesin                                                         AA
          protein [ECs2116] [Escherichia coli O157:H7]                     align

```

Score = 129 bits (323), Expect = 2e-28

Identities = 86/321 (26%), Positives = 156/321 (47%), Gaps = 19/321 (5%)

```

Query: 371 NAMIWRFMHNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPV 430
      N++   +H+RL P   +L   + S               +W+R + GH
Sbjct: 156 NSLFSHRLHDLRGEPQYTDLSHSQDSASS-----MWMRHVGGHERSSAGDQQLNT 205

```

Query: 431 EGYRKGVLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFHNPDNDLTTGNVKGFGAGVY 489
 + R +QLGG++ W N ++ +G+M G A Q S + + G + G+ AG+Y
 Sbjct: 206 QANRYVLQLGGDLAQWSSNAQDRWHLGVMAGYANQHSNTQSNRVGYKSDGRISGYSAGLY 265

Query: 490 ATWHQLQDKQTGAYADSWMQYQRFRRHINTED-GTERFTSKGITASIEAGYNALLAEHFT 548
 ATW+Q +TGAY DSW Y F ++++++ + + S+G+TAS+E GY
 Sbjct: 266 ATWYQNDANKTGAYVDSWALYNWFDNSVSSDNRSADDYDSRGVTASVEGGYTFEAGTCSG 325

Query: 549 KKGNSLRVYLQPQAQLTYLGV-NGKFSSENAHVNLGSRQLQTRVGQVQ----AKAQFSL 603
 +G Y+QPQAQ+T++GV + + + + G +QTR+GV+ + Q
 Sbjct: 326 SEGTLNTWYVQPQAQITWMGVKSDHARKDGTRIETEGDGNVQTRLGVKTYLNSHHQRDD 385

Query: 604 YKNIAIEPFAAVNALYHNKPFGVEMDGERRVINNKTAI-ESQLGVAVKIKSHLTLOATFN 662
 K +P+ N + ++K + V+M+G+ + + E + GV K+ ++L+L
 Sbjct: 386 GKQREFQPYIEANWINNSKVYAVKMNGQTVSRDGARNLGEVRTGVEAKVNNNLSLWGNVG 445

Query: 663 RQTG-KHHQAKQGALNLQWTF 682
 Q G K + QG L +++++
 Sbjct: 446 VQLGDKGYSDTQGM LGVKYSW 466

tr Q83LF4 Hypothetical protein SF1157 [SF1157] [Shigella flexneri] 773 AA align

Score = 128 bits (321), Expect = 4e-28

Identities = 139/563 (24%), Positives = 231/563 (40%), Gaps = 85/563 (15%)

Query: 174 LGPKIKNSHINSEILSVGNYTEWANQVIHH-----IENYVSFAAHLYSGLDPFHYI 224
 L I +ILS G+ AN++++H ++ VS AA ++ H
 Sbjct: 199 LESSINGQEATVDILS-GSSLRANEILYHKDETSNVTITDSEVSSAADVFNNIKGHILT 257

Query: 225 EVTDNSHVIGQT-ISLDEFR-----LENSLWEPRWDSNVGKLKT'TNADIRFN-----T 271
 NS + G IS D+ +NS W+ + DS V L N+ + +
 Sbjct: 258 VDATNSKITGSANISTDDNTHTYLSLSDNSTWDIKADSTVSNLTVDNSTVYISRADGRDV 317

Query: 272 KSESLLVKEDYAGG---ARFRFAYDPKEAKNTALIFEKNVTGTSDIIFENPIDD-LKSLD 327
 + L + E+Y G R D + ++ N +GT+ + N +L+
 Sbjct: 318 EPTRLTITENYVGNNGVHLRLTELDDDNSATDKVINGNTSGTTRVKVTNAGGSGAYTLN 377

Query: 328 GHQIIKVNGTAD----KHAFRLSGKHQ-----KGIYTLSQLQRPEGFLPKCKN 371
 G +II V G ++ K + +G ++ K Y + Q G +
 Sbjct: 378 GIEIISVEGESNGEFIKDSRIFAGAYEYSLTRGNTATNKNWYLTNFQATSGGETNSGGS 437

Query: 372 AMIWRFMHNRLKPPIPYCALRLNNKNSDIFDRTLPRKG-----LWLRVI 415
 + L+P L N+ R R G LWLR I
 Sbjct: 438 SAPTVAPTPVLRPEAGSYVANLAAANTLFVMRLNDRAGEMRYIDPVTEQERSRLWLRQI 497

Query: 416 DGHSNQWVQGTAPVEGYRKGVLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFHNPDND 474
 GH+ +R QLGG++ T +S+ +G+M G A + H+ +D
 Sbjct: 498 GGHNAWRDSNGQLRTTSHRYVSQLGDDLTTGGFTDSDSWRLGVMAGYARDYNLTHSSVSD 557

Query: 475 NLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRRHINTED-GTERFTSKGITA 533
 + G+V+G+ AG+YATW + GAY DSW QY F++ + ++ E +++KG T
 Sbjct: 558 YRSKGSVRGYSAGLYATWFADDISKKGAYIDSWAQYSWFKNSVKGDELAYESYSAKGATV 617

Query: 534 SIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSSENAHVNLGSR----- 587

```

      S+EAGY   L + F +           QPQAQ  ++GV+           NAH   GSR
Sbjct: 618 SLEAGYGFALNKSFGLEAAKYTWIFQPQAQAIWMGVD-----HNAHTEANGSRIENDAN 671

Query: 588 -QLQTRVG----VQAKAQFSLYKNIAIEPFPAAVNALYHNKPFVGVEMDG---ERRVINN-- 637
      +QTR+G    ++ + + S           EPF  +N ++++K F V M+G   E+  ++N
Sbjct: 672 NNIQTRLGFRTFIRTQEKNSGPHGDDFEPFVEMNWIHNSKDFAVSMNGVKVEQDGVSNLG 731

Query: 638 --KTAIESQLGVAVKIKSHLTLQ 658
      K +     L  A +  ++ +Q
Sbjct: 732 EIKLGVNGNLPAAASVWGNVGVQ 754

```

```

tr   Q7UCU4           Hypothetical protein [S1242] [Shigella flexneri] 773 AA
                                align

```

Score = 128 bits (321), Expect = 4e-28

Identities = 139/563 (24%), Positives = 231/563 (40%), Gaps = 85/563 (15%)

```

Query: 174 LGPKIKNSHINSEILSVGNYTEWANQVIHH-----IENYVSFAAHLYSGLDPFHYI 224
      L  I          +ILS G+   AN++++H           ++ VS AA ++   H
Sbjct: 199 LESSINGQEATVDILS-GSSLRANEILYHKDETSNVTITDSEVSSAADVFINNKGHLT 257

Query: 225 EVTDNSHVIGQT-ISLDEFR-----LENSLWEPRWDSNVGKLKTTNADIRFN-----T 271
      NS + G   IS D+           +NS W+ + DS V  L   N+ + +
Sbjct: 258 VDATNSKITGSANISTDDNTHTYLSLSDNSTWDIKADSTVSNLTVDNSTVYISRADGRDV 317

Query: 272 KSESLLVKEDYAGG---ARFRFAYDPKEAKNTALIFEKNVTGTSDIIFENPIDD-LKSLD 327
      +   L + E+Y G           R   D   +   ++   N +GT+ +   N           +L+
Sbjct: 318 EPTRLTITENYVGNGVLHLRTELDDDNSATDKVINGNTSGTTRVKVTNAGGSGAYTLN 377

Query: 328 GHQIIKVN GTAD----KHAFLRSGKHQ-----KGIYTLSLQQRPEGFLPKCKN 371
      G +II V G ++   K +   +G ++           K Y + Q   G   +
Sbjct: 378 GIEIISVEGESNGEFIKDSRIFAGAYEYSLTRGNTTEATNKNWYLTNFQATSGGETNSGGS 437

Query: 372 AMIWRFMHNRLKPPPIPYCALRLNKNKNSDIFDRTLPRKG-----LWLRVI 415
      +           L+P           L   N+   R   R G           LWLR I
Sbjct: 438 SAPTVAPTPVLRPEAGSYVANLAAANTLFVMRLNDRAGETRYIDPVTEQERSRLWLRQI 497

Query: 416 DGHSNQWVQKTPAVEGYRKGVLGGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFHNPD TD 474
      GH+           +R   QLGG++ T   +S+   +G+M G A   +   H+   +D
Sbjct: 498 GGHNAWRDSNGQLRTTSHRYVSQLGDDLTTGGFTDSDSWRLGVMAGYARDYNLTHSSVSD 557

Query: 475 NLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTED-GTERFTSKGITA 533
      + G+V+G+ AG+YATW           + GAY DSW QY  F++ +   ++   E +++KG T
Sbjct: 558 YRSKGSVRGYSAGLYATWFADDISKKGAYIDSWAQYSWFKNSVKGDELAYESYSAKGATV 617

Query: 534 SIEAGYNALLAEHFTTKGNSLRVYLQPQAQLTYLGVNGKFSDSENAHVNLLGSR----- 587
      S+EAGY   L + F +           QPQAQ  ++GV+           NAH   GSR
Sbjct: 618 SLEAGYGFALNKSFGLEAAKYTWIFQPQAQAIWMGVD-----HNAHTEANGSRIENDAN 671

Query: 588 -QLQTRVG----VQAKAQFSLYKNIAIEPFPAAVNALYHNKPFVGVEMDG---ERRVINN-- 637
      +QTR+G    ++ + + S           EPF  +N ++++K F V M+G   E+  ++N
Sbjct: 672 NNIQTRLGFRTFIRTQEKNSGPHGDDFEPFVEMNWIHNSKDFAVSMNGVKVEQDGVSNLG 731

Query: 638 --KTAIESQLGVAVKIKSHLTLQ 658
      K +     L  A +  ++ +Q

```

Sbjct: 732 EIKLGVNGNLPAAASVWGNVGVQ 754

tr Q9CKA8 **Hypothetical protein PM1717 [PM1717] [Pasteurella multocida]** 850 AA

align

Score = 126 bits (317), Expect = 1e-27

Identities = 117/434 (26%), Positives = 199/434 (44%), Gaps = 47/434 (10%)

Query: 274 ESLLVKEDYAG-----GARFRFAYDPKEAKNTALIFEKNVTGTSDIIFEN-PIDDLKS 325

+++ + EDY G A F +P + L N TG + + + D +

Sbjct: 429 KNVTINEDYQGHNGTLHLSADFNNGTTNPTDT---LFIRGNATGKTRVAIHIGADAENA 484

Query: 326 LDGHQIIKVNGTADKHAFRLSGKHQKGIYTLSSLQQRPE-----GFLPKCKNAM 373

++G +II+ N + D +AF + KG + L++R E G P + M

Sbjct: 485 VNGVKIIETNTSTD-NAFVIDNYLSKGAFFVYHLEKRHETNQDNWYLTSYIGGTPSYRAEM 543

Query: 374 IWRFMHNRLKPPPIPYCALRLNNKNS-DIFDRTLPRKGLWLRVIDGHSNQWVQGTAPVEG 432

N L LRL ++ S F K W+R ++G ++ ++ +

Sbjct: 544 A--SYANNLYAAHQFLQLRLEDRLSRHHFLNQSADKTFWIRAVEGTNHNMRDNQNTTKA 601

Query: 433 YRKGVLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDNDNLTTGNVKGFGAGVYATW 492

R QLG V N+++ + G+M G A+Q S + + G V+G+ G VY TW

Sbjct: 602 QRYVTQLGKTVI---NQAHYHA-GVMFGYAKQSSKTRSSRVGT-SRGKVQGYALGVYGTW 656

Query: 493 HQLQDKQTGAYADSWMQYQFRHR-INTEDGTERFTSKGITASIEAGYNALLAEHFTKKG 551

+Q + TG Y DSW+QYQ F+++ IN ++ + ++G++AS+E GY+ L + +T

Sbjct: 657 YQNPNDTGLYIDSWLQYQWFKNQVINPASSSDNYRTQGLSASLELGYHLPLVQ-YTVAD 715

Query: 552 NSLRVYLQPPAQQLTYLGVNGK-FSDSENAHVNLGSRQLQTRVGVQAKAQFSLYKNIA-- 608

+ +QPQAQ + +N K D + ++ +G + QTR+GV +FSL +

Sbjct: 716 LKHSLNIQPPAQFIWQKLNSKQHRDPQOTLIHYIGQONTQTRLGV---RFSLDHFLNT 771

Query: 609 ---IEPFAAVNALYHNKPFVEM-DGERRVINNKTAIESQLGVAVKIKSHLTLQATFNQ 664

++P+ VN L+H K +G+ + D + K E + G+A + HL Q

Sbjct: 772 QWNLPYPFEVNWHLHAKDYGITINDVVNHIEGAKQLFEYKAGIASQFGRHLRFWLDTHQ 831

Query: 665 TGKHHQAKQGALNL 678

GK Q K LN+

Sbjct: 832 RGK-QQFKDNQLNV 844

tr P75997 **Putative part of putative ATP-binding component of a transport system [b1170] [Escherichia coli K12]** 338 AA

align

Score = 118 bits (296), Expect = 3e-25

Identities = 76/234 (32%), Positives = 119/234 (50%), Gaps = 19/234 (8%)

Query: 410 LWLRVIDGHSNQWVQGTAPVEGYRKGVLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTF 468

LWLR I GH+ +R QLGG++ T +S+ +G+M G A +

Sbjct: 66 LWLRQIGGHNAWRDSNGQLRTTSHRYVSQLGGDLLTGGFTDSDSWRLGVMAGYARDYNLT 125

Query: 469 HNPDTNDLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTED-GTERFT 527

```

      H+  +D  + G+V+G+ AG+YATW      + GAY DSW QY  F++ +  ++  E ++
Sbjct: 126 HSSVSDYRSKGSVRGYSAGLYATWFADDISKKGAYIDSWAQYSWFKNSVKGDELAYESYS 185

Query: 528 SKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDSENAHVNLGSR 587
      +KG T S+EAGY  L + F  +      QPQAQ  ++GV+      NAH  GSR
Sbjct: 186 AKGATVSLEAGYG FALNKSFGLEAAKYTWIFQPQAQAIWMGVD-----HNAHTEANGSR 239

Query: 588 -----QLQTRVG-----VQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDG 630
      +QTR+G      ++ + + S      EPF  +N ++++K F V M+G
Sbjct: 240 IENDANNNIQTRLGFRTFIRTQEKNSGPHGDDFEPFVEMNWIHNSKDFAVSMNG 293

```

```

sp      Q03155      Adhesin aidA-I precursor [aidA-I] [Escherichia 1286 AA
      AIDA_ECOLI      coli]      align

```

Score = 118 bits (295), Expect = 4e-25

Identities = 105/414 (25%), Positives = 186/414 (44%), Gaps = 40/414 (9%)

```

Query: 302 LIFEKNVTGTSDIIFENPIDDL-KSLDGHQIIKVNGTADKHAFLSGKHQKGIYTLSQLQ 360
      L+ + N +G SDI++ N      ++ DG  II V G +D  F L  +  G Y  +LQ+
Sbjct: 880 LVVKGNTSGQSDIVYVNEDGSGGQTRDGINIISVEGNSDAE-FSLKNRVVAGAYDYTLQK 938

Query: 361 RPEGFLPKCKNAMIWRFMH-----NRLKPPIPYCALRLNNKNS-----DIF 401
      E      N  +  H      + +P  · A  +  NS      +
Sbjct: 939 GNES---GTDNKGWYLTSHLPTS DTRQYRPENGSYATNMALANSLFLMDLNERKQFRAMS 995

Query: 402 DRTLPRKG-LWLRVIDGHSNQWV---QGKTAPVEGYRKGVLGGGEVFTWQNES-NQLSIG 456
      D T P  +W+++  G S+  +  Q KT  +      QLGG+++ +  E      ++G
Sbjct: 996 DNTQPESASVWMKITGGISSGKLNDGQNKTTTNQFIN---QLGGDIYKFHAEQLGDFTLG 1052

Query: 457 LMGGQAEQRSTFHNPD TDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFHRH 516
      +MGG A  +      N  ++      + G+  G VY TW+Q  +  TG +A++WMQY  F
Sbjct: 1053 IMGGYANAKGKTINYTSNKAARNTLDGYSVGVYGTWYQNGENATGLFAETWMQYNWFNAS 1112

Query: 517 INTED-GTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSD 575
      +  +      E++  G+TAS  GYN  +      + +G  +  +LQP  Q  ++GV
Sbjct: 1113 VKGDGLEEEKYNLNLGTASAGGGYNLNVHTWTSPEGITGEFWLQPHLQAVWMGVTPDTHQ 1172

Query: 576 SENAH-VNLLGSRQLQTRVGVQA--KAQFSLYKNIA--IEPFAAVNALYHNKPFGVEMDG 630
      +N  V  G  +QT+ G++A  K  + +L K+      P+  N  +++  FGV+M
Sbjct: 1173 EDNGTVVQGAGKNNIQTKAGIRASWKVKSTLDDKTGRRFRPYIEANWIHNTHFEGVKMSD 1232

Query: 631 ERRVIN-NKTAIESQLGVAVKIKSHLTLQATFNRTGKH-HQAKQGALNLQWTF 682
      + ++++ ++  E + G+  I  +L++      Q G H  A  GAL  ++++F
Sbjct: 1233 DSQLLSGSRNQGEIKTGIEGVITQNLVNGGVAYQAGGHGSNAISGALGIKYSF 1286

```

```

tr      Q7CPG9      Putative autotransported protein [misL] [Salmonella 955
      typhimurium]      AA
                        align

```

Score = 110 bits (276), Expect = 7e-23

Identities = 81/286 (28%), Positives = 142/286 (49%), Gaps = 22/286 (7%)

```

Query: 410 LWLRVIDGHS--NQWVQGKTAPVEGYRKGVLGGGEVFTWQNES-NQLSIGLMGGQAEQRS 466

```

```

      LW+R + H+ N      + Y  +QLGG++ W + ++ IG M G A ++
Sbjct: 679 LWMRNVGAHTRFNDGSGQLKTRINSYV--LQLGGDLAQWSTDGLDRWHIGAMAGYANSQN 736

Query: 467 TFHNPDTDNLTGTVKGFAGVYATWHQLQDKQTGAYADSWMQYQRFHRINTED-GTER 525
      + +D + G V G+ G+Y TW+      ++GAY D+WM Y F +++ +D E+
Sbjct: 737 RTLSSVSDYHSRGQVTGYSVGLYGTWYANNIDRSYGAYVDTWMLYNWFDNKVMGQDQAAEK 796

Query: 526 FTSKGITASIEAGYNALLAEHFTKKGNLSRVYLQPQAQLTYLGVNGKFSDSENAHVNLL- 584
      + SKGITAS+EAGY+ L E +      +LQP+AQ+ ++GV      D+ A+ L+
Sbjct: 797 YKSKGITASVEAGYSFRLGESAHQS-----YWLQPKAQVVMGMVQA--DDNREANGTLVK 849

Query: 585 --GSRQLQTRVGVOAKAQ----FSLYKNIAIEPFAAVNALYHNKPFGVEMDG-ERRVINN 637
      + L TR+GV+A      K+ +PF N +++ +P V+MD      +
Sbjct: 850 DDTAGNLLTRMGVKAYINGHNAIDNDKSREFQPFVEANWIHNTQPASVKMDDVSSDMRG 909

Query: 638 KTAIESQLGVAVKIKSHLTLQATFNRTG-KHHQAKQGALNLQWTF 682
      K E ++G+ ++ L +      +Q G +      QG L ++++F
Sbjct: 910 KNIGELKVGIEGQVTPRLNVWGNVAQQVGDGTGYSDTQGMLGMKYSF 955

```

```

tr    Q9Z625      MisL [misL] [Salmonella typhimurium]      955 AA
                                align

```

Score = 110 bits (276), Expect = 7e-23

Identities = 81/286 (28%), Positives = 142/286 (49%), Gaps = 22/286 (7%)

```

Query: 410 LWLRVIDGHS--NQWVQKTAPEVEGYRKGVLGGEVFTWQNES-NQLSIGLMGGQAEQRS 466
      LW+R + H+ N      + Y  +QLGG++ W + ++ IG M G A ++
Sbjct: 679 LWMRNVGAHTRFNDGSGQLKTRINSYV--LQLGGDLAQWSTDGLDRWHIGAMAGYANSQN 736

Query: 467 TFHNPDTDNLTGTVKGFAGVYATWHQLQDKQTGAYADSWMQYQRFHRINTED-GTER 525
      + +D + G V G+ G+Y TW+      ++GAY D+WM Y F +++ +D E+
Sbjct: 737 RTLSSVSDYHSRGQVTGYSVGLYGTWYANNIDRSYGAYVDTWMLYNWFDNKVMGQDQAAEK 796

Query: 526 FTSKGITASIEAGYNALLAEHFTKKGNLSRVYLQPQAQLTYLGVNGKFSDSENAHVNLL- 584
      + SKGITAS+EAGY+ L E +      +LQP+AQ+ ++GV      D+ A+ L+
Sbjct: 797 YKSKGITASVEAGYSFRLGESAHQS-----YWLQPKAQVVMGMVQA--DDNREANGTLVK 849

Query: 585 --GSRQLQTRVGVOAKAQ----FSLYKNIAIEPFAAVNALYHNKPFGVEMDG-ERRVINN 637
      + L TR+GV+A      K+ +PF N +++ +P V+MD      +
Sbjct: 850 DDTAGNLLTRMGVKAYINGHNAIDNDKSREFQPFVEANWIHNTQPASVKMDDVSSDMRG 909

Query: 638 KTAIESQLGVAVKIKSHLTLQATFNRTG-KHHQAKQGALNLQWTF 682
      K E ++G+ ++ L +      +Q G +      QG L ++++F
Sbjct: 910 KNIGELKVGIEGQVTPRLNVWGNVAQQVGDGTGYSDTQGMLGMKYSF 955

```

```

sp    P45508      Hypothetical protein yfaL precursor [yfaL] [Escherichia coli] 1250
      YFAL_ECOLI  coli]
                                AA
                                align

```

Score = 96.3 bits (238), Expect = 2e-18

Identities = 74/279 (26%), Positives = 136/279 (48%), Gaps = 27/279 (9%)

```

Query: 412 LRVIDGHSNQWVQKTAPEVEGYRKGVLGGEVFT--WQNESNQLSIGLMGGQAEQRSTFH 469

```

```

      LRVI G +      G+ A E      VQL G++F+ W + + +G++GG ++ +
Sbjct: 989 LRVIGGDYHYTAAGQLAQHED-TSTVQLSGDLFSGRWGTDGEWM-LGIVGGYSDNQGDSDR 1046

Query: 470 NPDTDNLTGNGVKGFGAGVYATWHQLQDKQKTGAYADSWMQYQRFHRIN-TEDGTERFTS 528
      + T      G+ G+ ++W Q +++ GA+ DSW+QY F + ++ EDGT+ + S
Sbjct: 1047 SNMTGTRADNQNHGYAVGLTSSWFQHGNGKQKQGAWLDSWLQYAWFSNDVSEQEDGTDHYHS 1106

Query: 529 KGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV-NGKFSDSENAHVNLGSR 587
      GI AS+EAGY L      V ++PQAQ+ Y GV      F+ + A V+
Sbjct: 1107 SGIIASLEAGYQWLPGR-----GVVIEPQAQVIYQGVQDDFTAANRARVSQSQGD 1157

Query: 588 QLQTRVG VQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGERRVINN---KTAIESQ 644
      +QTR+G+ ++ +      A+      ++ Y++ P      E++ +      I++ K      E +
Sbjct: 1158 DIQTRLGLHSEWR-----TAVHVIPTLDLNYHDPHSTEIEEDGSTISDDAVKQGEIK 1211

Query: 645 LGVAVKIKSHLTLQATFNRTGKHHQAKQG---ALNLQW 680
      +GV I      ++L+ +      Q G      A+      ++ ++W
Sbjct: 1212 VGVGTGNISQVRSLRGSVAWQKGSDDFAQTAGFLSMTVKW 1250

```

tr Q8ZN57 Similar to the C-terminal region of AIDA [shdA] [Salmonella 2039 AA typhimurium]

align

Score = 95.5 bits (236), Expect = 3e-18

Identities = 75/289 (25%), Positives = 128/289 (43%), Gaps = 29/289 (10%)

```

Query: 410 LWLRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFH 469
      +W R      G +      ++      QLGG++ W N      +++G+M      +++
Sbjct: 1764 VWARFKAGKAESEAVSGNIDMDSNYSQFQLGGDILAWGNGQQSVTVGVM-----ASYI 1816

Query: 470 NPDTDNL-----TTGNGVKGFGAGVYATWHQLQDKQKTGAYADSWMQYQRFHRIN 518
      N DTD+      ++GNV G+      G VYATW      +GAY DSW QY + + +
Sbjct: 1817 NADTDSTGNRGADGSQFTSSGNVDGYNLGVYATWFADAQTHSGAYVDSWYQYGFYNNNSVE 1876

Query: 519 TED-GTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNG-KFSDS 576
      + D G+E + S      S+E GY      +A      GN+ V L PQAQ+ + +      D+
Sbjct: 1877 SGDAGSESYDSTANAVSLETGYRYDIA---LSNGNT--VSLTPQAQVWQNYSDSVKDN 1931

Query: 577 ENAHVNLLGSRQLQTRVG VQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGERRVIN 636
      ++      TR+G++ +      I+PFA N L+ +      V D + V
Sbjct: 1932 YGTRIDGQDGDSWTTTLGLRVDGKLYKGSRTVIQPF AEANWLHTSDDVSVSFD-DATVKQ 1990

Query: 637 NKTA--IESQLGVAVKIKSHLTLQATFNRTGKHHQAK-QGALNLQWTF 682
      + A      E ++G+ I      +++A      QTG +      G+LNL++ +
Sbjct: 1991 DLPANRAELKVGLQADIDKQWSVRAQVAGQTGSNDFGDLNGSLNLRYNW 2039

```

tr Q8CVV7 Hypothetical protein yfaL [yfaL] [Escherichia coli 1254 AA 06]

align

Score = 95.5 bits (236), Expect = 3e-18

Identities = 71/278 (25%), Positives = 138/278 (49%), Gaps = 25/278 (8%)

```

Query: 412 LRVIDGHSNQWVQGKTAPVEGYRKGVQLGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFHN 470

```

```

          LRVI G +      G+ A E      VQL G +F+      + + +G++GG ++ +      +
Sbjct: 993 LRVIGGRYHYTAVGQLAQHED-TSTVQLSGNLFSGHWGDDGEWMLGIVGGYSDNQGDSRS 1051

Query: 471 PDTDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRRHRIN-TEDGTERFTSK 529
          T          G+  G+ ++W+Q  +++ GA+ DSW+QY  F + ++ +DG + + S
Sbjct: 1052 NMTGTRADNQNHGYAVGLTSSWYQHGNQKQGAWLDSWLQYAWFNNDVSEQDDGVDHYHSS 1111

Query: 530 GITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV-NGKFSDSENAHVNLLGSRQ 588
          GI AS+EAGY  L          V ++PQAQ+ Y GV      F+ + +A V+
Sbjct: 1112 GIIASLEAGYQWLPGR-----GVVIEPQAQVIYQGVQDDFTAANHARVSQSQGD 1162

Query: 589 LQTRVGQAKAQFSLYKNIAIEPFAAVNALYHNKPFGEVMDGERRVINNKTAI---ESQL 645
          +QTR+G+ ++ + +      +++ P  +N  Y++ P  E++ +  I++  A  E ++
Sbjct: 1163 IQTRLGLHSEWRTA----VSVTPTLDLN--YYHDPHATEIEEDGSTISDDAAKQRGEIKV 1216

Query: 646 GVAVKIKSHLTLQATFNRQTGKHHQAKQG---ALNLQW 680
          G+  I  ++L+ +  Q G  A+      ++ ++W
Sbjct: 1217 GITGNISQRVSLRGSVAWQKGSDDFAQTAGFLSMTVKW 1254

```

```

tr    Q9XCJ4          ShdA [shdA] [Salmonella typhimurium]          2035 AA
                                           align

```

Score = 95.5 bits (236), Expect = 3e-18

Identities = 75/289 (25%), Positives = 128/289 (43%), Gaps = 29/289 (10%)

```

Query: 410 LWLRVIDGHSNQWVQKTAPVEGYRKGVLGGGEVFTWQNESNQLSIGLMGGQAEQRSTFH 469
          +W R  G +          ++      QLGG++  W N      +++G+M      +++
Sbjct: 1760 VWARFKAGKAESEAVSGNIDMSNYSQFQLGGDILAWGNGQQSVTVGVM-----ASYI 1812

Query: 470 NPDTDNL-----TTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRRHRIN 518
          N DTD+          ++GNV G+  GVIATW          +GAY DSW QY  + + +
Sbjct: 1813 NADTDSTGNRGADGSQFTSSGNVDGYNLGVYATWFADAQTHSGAYVDSWYQYGFYNNNSVE 1872

Query: 519 TED-GTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNG-KFSDS 576
          + D G+E + S      S+E GY  +A      GN+  V L PQAQ+ +  +  D+
Sbjct: 1873 SGDAGESYDSTANAVSLETGYRYDIA--LSNGNT--VSLTPQAQVWQNYADSVDKDN 1927

Query: 577 ENAHVNLLGSRQLQTRVGQAKAQFSLYKNIAIEPFAAVNALYHNKPFGEVMDGERRVIN 636
          ++          TR+G++  +          I+PFA  N L+ +  V  D +  V
Sbjct: 1928 YGTRIDGQDGDSWTTRLGLRVDGKLYKGSRTVIQPF AEANWLHTSDDVSVSFD-DATVKQ 1986

Query: 637 NKTA--IESQLGVAVKIKSHLTLQATFNRQTGKHHQAK-QGALNLQWTF 682
          +  A  E ++G+  I      +++A  QTG +      G+LNL++ +
Sbjct: 1987 DLPANRAELKVGLQADIDKQWSVRAQVAGQTGSNDFGDLNGLSLNLRYNW 2035

```

```

tr    Q8XE28  Putative ATP-binding component of a transport system [yfaL] 1250 AA
          [Escherichia coli O157:H7]
                                           align

```

Score = 93.2 bits (230), Expect = 1e-17

Identities = 72/279 (25%), Positives = 134/279 (47%), Gaps = 27/279 (9%)

```

Query: 412 LRVIDGHSNQWVQKTAPVEGYRKGVLGGGEVFT--WQNESNQLSIGLMGGQAEQRSTFH 469

```

```

          LRVI G +   G+ A E   VQL G++F+ W +   + +G++GG ++ +
Sbjct: 989  LRVIGGDYHYTAAGQLAQHED-TSTVQLSGDLFSGRWGTDGEWM-LGIVGGYSDNQGDSR 1046

Query: 470  NPDTDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFHRINT-EDGTERFTS 528
          + T           G+ G+ ++W Q   ++ GA+ D+W+QY F + ++ EDG + + S
Sbjct: 1047 SSMTGTRADNQNHHGYAVGLTSSWFQHGKQKQGAWLNDNLQYAWFSNDVSEHEDGVDHYHS 1106

Query: 529  KGITASIEAGYNALLAEHFTTKGNSLRVYLQPQAQLTYLGV-NGKFSDSENAHVNLGSR 587
          GI AS+EAGY L           V ++PQAQ+ Y GV   F+ + A V+
Sbjct: 1107 SGIIASLEAGYQWLPGR-----GVVIEPQAQVIYQGVQDDFTAAANRARVSQSQGD 1157

Query: 588  QLQTRVGQVQAKAQFSLYKNIAIEPFAAVNALYHNKPFVEMDGERRVINN---KTAIESQ 644
          +QTR+G+ ++ +   A+   ++ Y++ P   E++ +   I++ K   E +
Sbjct: 1158 DIQTRLGLHSEWR-----TAVHVIPTLDLNYHDPHSTEIEEDASTISDDAVKQGEIK 1211

Query: 645  LGVAVKIKSHLTLQATFNRQTGKHHQAKQG---ALNLQW 680
          +GV I   ++L+ +   Q G   A+   ++ ++W
Sbjct: 1212 VGVGTGNISQVRSLRGSVAWQKGSDDFAQTAGFLSMTVKW 1250

```

```

tr  Q7AC44  Putative ATP-binding component of a transport system      1250
          [ECs3116]                                                    AA
          [Escherichia coli O157:H7]                                   align

```

Score = 93.2 bits (230), Expect = 1e-17

Identities = 72/279 (25%), Positives = 134/279 (47%), Gaps = 27/279 (9%)

```

Query: 412  LRVIDGHSNQWVQKTAPEGYRKGVLGGEVFT--WQNESNQLSIGLMGGQAEQRSTFH 469
          LRVI G +   G+ A E   VQL G++F+ W +   + +G++GG ++ +
Sbjct: 989  LRVIGGDYHYTAAGQLAQHED-TSTVQLSGDLFSGRWGTDGEWM-LGIVGGYSDNQGDSR 1046

Query: 470  NPDTDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFHRINT-EDGTERFTS 528
          + T           G+ G+ ++W Q   ++ GA+ D+W+QY F + ++ EDG + + S
Sbjct: 1047 SSMTGTRADNQNHHGYAVGLTSSWFQHGKQKQGAWLNDNLQYAWFSNDVSEHEDGVDHYHS 1106

Query: 529  KGITASIEAGYNALLAEHFTTKGNSLRVYLQPQAQLTYLGV-NGKFSDSENAHVNLGSR 587
          GI AS+EAGY L           V ++PQAQ+ Y GV   F+ + A V+
Sbjct: 1107 SGIIASLEAGYQWLPGR-----GVVIEPQAQVIYQGVQDDFTAAANRARVSQSQGD 1157

Query: 588  QLQTRVGQVQAKAQFSLYKNIAIEPFAAVNALYHNKPFVEMDGERRVINN---KTAIESQ 644
          +QTR+G+ ++ +   A+   ++ Y++ P   E++ +   I++ K   E +
Sbjct: 1158 DIQTRLGLHSEWR-----TAVHVIPTLDLNYHDPHSTEIEEDASTISDDAVKQGEIK 1211

Query: 645  LGVAVKIKSHLTLQATFNRQTGKHHQAKQG---ALNLQW 680
          +GV I   ++L+ +   Q G   A+   ++ ++W
Sbjct: 1212 VGVGTGNISQVRSLRGSVAWQKGSDDFAQTAGFLSMTVKW 1250

```

```

tr  Q9FCW0  Hypothetical protein [Kluyvera ascorbata]      652 AA
                                         align

```

Score = 73.9 bits (180), Expect = 9e-12

Identities = 76/299 (25%), Positives = 123/299 (40%), Gaps = 44/299 (14%)

```

Query: 246  NSLWEPRWDSNVGKLKTTNADIRFNTKSES--LLVKEDYAGG---ARFRFAYDPKEAKNT 300

```

```

      NSLW+   DS +   L   N   +   +   S   L   V   +Y G   R   +
Sbjct: 361 NSLWKMTGDSVLSSLTLNNGTVEWAGASAGNVLTVAGNYQGNGLLRINTVLGDDNSVTD 420

Query: 301 ALIFEKNVTGTSDIIFENPIDDL-KSLDGHQIIKVNGTADKHAFLRLSGKHQKGIYTLSLQ 359
      L+ E + +GT+ +   N   K+++G ++I V+G +D + F   SG+   G Y   +L+
Sbjct: 421 KLVVEGDTSGTTFVAVTNAGGSGDKTINGIEVIHVDGASDGN-FVQSGRIVAGSYEYALR 479

Query: 360 QRPEGFLPKCKNAMIWRFMHNRLKP--PIP-----YCALRLNNKNSDIFDRTLTP 406
      R EG           W M+   P   P+P           Y A L   N+   R
Sbjct: 480 -RGEGTAFNH-----WYLMNAATTPEEPVPEKPTLRPESGSYIA-NLAAANTMFTTRLHD 532

Query: 407 RKG-----LWLRVIDGHSNQWVQGKTAPVEGYRKGVLGGGEVFTWQ-NE 449
      R G           +W+R + GH+           + R +QLGG++ W N
Sbjct: 533 RLGETQYIARLTGEQKVTSMWMNRNVGGHTRFKDSSGQLSTQSNRYVLQLGGDIAQWSTNG 592

Query: 450 SNQLSIGLMGGQAEQRSTFHNPDNDLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWM 508
      ++ +GLM G   +S   +   +   + G V G+ AG+Y TW+   +   +TG+Y DSW+
Sbjct: 593 LDRWHLGLMAGYGNSQSNTKSDVSRYHSRGQVTGYSAGIYGTWYANEADKTGSYLD SWI 651

```

tr Q6IU25 **YdeU (Fragment) [Escherichia coli B]** 169 AA
align

Score = 70.5 bits (171), Expect = 1e-10

Identities = 39/138 (28%), Positives = 63/138 (45%), Gaps = 11/138 (7%)

```

Query: 371 NAMIWRFMHNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPV 430
      N++   +H+RL P           + +D           +W+R + GH
Sbjct: 41  NSLFSHRLHDLRLGEP-----QYTDLSHSQGSASSMWMRHVGGHERSRAGDQQLNT 90

Query: 431 EGYRKGVLGGGEVFTWQ-NESNQLSIGLMGGQAEQRSTFHNPDNDLTTGNVKGFGAGVY 489
      + R +QLGG++ W N ++ +G+M G A Q S   +           + G + G+ AG+Y
Sbjct: 91  QANRYVLQLGGDLAQWSSNAQDRWHLGVMAGYANQHSNTQSNRVGYKSDGRISGYAGLY 150

Query: 490 ATWHQLQDKQTGAYADSW 507
      ATW+Q   +TGAY DSW
Sbjct: 151 ATWYQNDANKTGAYVDSW 168

```

tr Q88LP9 **Outer membrane autotransporter [PP1880] [Pseudomonas putida** 730
 (strain AA
 KT2440)] align

Score = 66.2 bits (160), Expect = 2e-09

Identities = 109/474 (22%), Positives = 183/474 (37%), Gaps = 84/474 (17%)

```

Query: 228 DNSHVIGQTIS-----LDEF-----RLENSL-----WEPRWDSNVGKLKTTN 264
      +NSH++G ++           L+ F   RL+N           W   +S V L   N
Sbjct: 257 NNSHLVGDIVAASGGTANVLLENFATLKGRLDNVASLEINSGGEWTLVDNSQVTDLSLDN 316

Query: 265 ADIRFNTKSESLLVK-EDYAGGARFRFAYDPKEAKNTALIFEKNVTGTSD-----IIFEN 318
      +RF   E   + E+ G   F   D   +++ L   +VTGT+   +I   +
Sbjct: 317 GAVRFGGPGFEFFTLSENLTGNGT FIMEADFSTSQSDFL----DVTGTASGNHQLLISAS 372

Query: 319 PIDDLKSLDGHQIIKVNGTADKHAFLRLSGKHQKGIYTLSLQQRPEG-----FLPK 368

```

```

      D L      H +      G D      L G      G Y+ L Q R +      P
Sbjct: 373 GNDPLTDNSLHVHTAAG--DSQFSLGGSVDLGAYSVDLVQRGDNDWYLDATTRTVSPG 430

Query: 369 CKNAMIWRFMHNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVGKT- 427
      + M      + P I Y L +      R      + G W+R      + NQ+      T
Sbjct: 431 TQTMALA----NVVPTIWYGELGVLRSRMGDVRRNPGKAGGWVR---SYGNQFNVSATS 483

Query: 428 -APVEGYRKGVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDNDNLTTGN---VKG 483
      A + ++G+ +G +      + N L +G+ G      + N D NL G+ V
Sbjct: 484 GAAYQQQQGLSIGADAPLAAGDGNWL-VGITAG-----YSNSDL-NLARGSSASVDS 534

Query: 484 FGAGVYATWHQLQDKQTGAYADSWMQYQFRHR--INTEDGTER---FTSKGITASIEAG 538
      + AG YATW      D ++G Y D+ + RFR++ + DG++      +++ G S+E G
Sbjct: 535 YHAGAYATW---LDPESGYIIDTVARINRFRNQADVRLSDGSKAKGDYSNLGAGVSLEVG 591

Query: 539 YNALLAEHFTKKGNLSRVYLQPQAQLTYLGVNGK-FSDSENAHVNLLGSRQLQTRVGVQA 597
      + LA+ +      +L+P AQL+ L V GK +S      N      + L +VG
Sbjct: 592 RHLNLADDW-----FLEPFAQLSGLVVQGGKDYSLDNGMRANSNSTHSLGKVGTSV 642

Query: 598 KAQFSLYKNIAIEPFAAVNALYHNKPFGEVMDGERRVINNKTAIESQLGVAVKI 651
      FS      +++P+ V A++      + R +N      +++G V +
Sbjct: 643 GRTFSAGTGRSVQPYLRVAAVHEFVNDNQVKVNDNRFSSNLAGSRAEIGAGVAV 696

```

```

tr Q884S7 Autotransporter, putative [PSPTO2011] [Pseudomonas syringae] 769
      (pv. AA
      tomato)] align

```

Score = 66.2 bits (160), Expect = 2e-09

Identities = 105/460 (22%), Positives = 184/460 (39%), Gaps = 58/460 (12%)

```

Query: 249 WEPRWDSNVGKLKTTNADIRFNTKSESLLVKEDYAGGARFRFAYDPKEAKNTALIFEKNV 308
      W+ + D+ V L      + F +      L      +G F      D A      +
Sbjct: 342 WQMQGDNAVTSLSMQGGSVGFGEFHTLSLNELSGSGTFGLRVDLDNAVGDNLINVGQA 401

Query: 309 TGTSDIIFENPIDDLKSLDGHQIIKVNGT--ADKHAFRLSGKHQKGIYTLSQLQRPEGFL 366
      +G + N      ++ S D Q +KV T D      L G+ G Y+ L+Q+ +
Sbjct: 402 SQQFGLRVRNTGVEVISAD-MQPLKVVHTEGGDAQFSLGGRVDLGAYSYLLEQQGNDWF 460

Query: 367 PKCKNAMIWRFMHNRLK----PPIPYCALR-LNNKNSDIFDRTLPRKGLWLRVIDGHSN 420
      ++ +I      + L      P I      L L ++ ++ R      + G W+R      N
Sbjct: 461 VVGRDKVISPSTQSALALYSAAPAIWMSELSTLRSRMGEV--RASGQAGGWMRAYGSRLN 518

Query: 421 QWVGKGTAPVEGYRK--GVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDNDNL 477
      T+      YR+      G+ LG +      + + +L +G++GG +      + D T
Sbjct: 519 ----ATTSDGVDYRQKQSGLSLGADAPV-EVSNRLLVGVLGGYSTS-----DLDVDSRGT 568

Query: 478 TGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQFRHR--INTEDGTER---FTSKGIT 532
      TG V + AG Y TW L D      G Y D ++ RFR++ + D ++      +++ G+
Sbjct: 569 TGKVASYYAGAYGTW--LSD--DGYVVDGVLLKLNFRNKADVAMS DASKAKGDYSNTGVG 624

Query: 533 ASIEAGYNALLAEHFTKKGNLSRVYLQPQAQLTYLGVNGKFSDSENAHVNLLGSRQLQTR 592
      +EAG + LA+ +      +L+P AQL+ + V G+      +N      + ++ +TR
Sbjct: 625 GWVEAGRHIKLADDY-----FLEPFAQLSSVVVQGGELRLDNG----MKAKNARTR 671

Query: 593 VGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFGEVMDGERRVINNKTAIESQL----- 645

```

V K SL + +A++ V Y E V N ++ L
 Sbjct: 672 -SVLGKVGTSIGRTVALKD-GGVLQPYVRVAVAQEFSSRRNEVKANDVKFDNSLFGSRGEL 729
 Query: 646 --GVAVKIKSHLTQATFNRTGKHHQAKQGA-LNLQWTF 682
 GV+V + L L A + G+H + GA + L+ TF
 Sbjct: 730 GAGVSVSLSERLKLHADVDYMKGQHIEQPWGANVGLRLTF 769

tr Q7VYJ2 **Autotransporter [BP1344] [Bordetella pertussis]** 866 AA
align

Score = 65.5 bits (158), Expect = 3e-09

Identities = 79/308 (25%), Positives = 131/308 (41%), Gaps = 46/308 (14%)

Query: 397 NSDIFDRTLPRKGLWLRVIDGHSNQWVQGTAP-VEGYRKGVLGGEVFTW-QNESNQLS 454
 N + R R W R G+S Q + G P ++ GVQLG ++++ + + Q
 Sbjct: 583 NQALLARDGERVAAWARAYGCNSKQALDGDGAQPGIDARLAGVQLGQDLYSSVRPDGGQHR 642
 Query: 455 IGLMGGQAEQRSTFHN--DTDNLTGTG--VKGFGAGVYATWHQLQDKQTGAY-ADSWMQ 509
 GL GG + R H + TG + G+ G Y T+ + A A++WM
 Sbjct: 643 FGLFGGYGQARGDTHGSAGGERDAATGRLTIDGYSVGGYWTYVGPRGWYVDAVLANTWMD 702
 Query: 510 YQRFRRHINTEDGTERFT-SKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTY-- 566
 +++ G + T + TAS+E+GY L+E +T L+PQAQL Y
 Sbjct: 703 IDT-----DSKAGRDADTRGQAFTASLESGYPLALSERWT-----LEPQAQLIYQH 748
 Query: 567 LGVNGKFSDSENAHVNLLGSRQLQTRVGVAQAQFSLYKNIAIEPFAAVNALYHNKPFQV 626
 V+G FSD+ + V + L R+G + + +++ + P+AA+N F
 Sbjct: 749 TRVDG-FSDAV-SEVRIRDDNALTARLGARLQGEYAAAAQV-WRPYAALN-----FWR 798
 Query: 627 EMDGERRVI-----NNKTAIESQLGVAVKIKSHLTQATFNRTGKHHQAKQGA-- 675
 GE V+ T++E G +V + L L T Q +GA
 Sbjct: 799 TFSGENTVVLGEDSIDTRRGATSLELAAGASVTLARSLALYGRLAYATSIDSQYLRGASA 858
 Query: 676 -LNLQWTF 682
 L +++T+
 Sbjct: 859 QLGMRYTW 866

tr Q7WIM1 **Putative autotransporter [BB2830] [Bordetella bronchiseptica]** 849 AA
 (Alcaligenes bronchisepticus)]
align

Score = 64.3 bits (155), Expect = 7e-09

Identities = 75/304 (24%), Positives = 125/304 (40%), Gaps = 38/304 (12%)

Query: 397 NSDIFDRTLPRKGLWLRVIDGHSNQWVQGTAP-VEGYRKGVLGGEVFTW-QNESNQLS 454
 N + R R W R G+S Q + G P ++ GVQLG ++++ + + Q
 Sbjct: 566 NQALLARDGERVAAWARAYGCNSKQALDGDGAQPGIDARLAGVQLGQDLYSSVRPDGGQHR 625
 Query: 455 IGLMGGQAEQRSTFHN--DTDNLTGTG--VKGFGAGVYATWHQLQDKQTGAYADSWMQYQR 512
 GL GG R H + TG + G V W + + G Y D+ +
 Sbjct: 626 FGLFGGYGHARGDTHGSAGGERDAATGRLTIDGYSVGGYWTYVGPR--GWYVDTVLANW 683
 Query: 513 FRHRINTEDGTERFT-SKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVN- 570

```

      +++ G + T + +TAS+E+GY L+E +T L+PQAQL Y
Sbjct: 684 MDIDTDSKAGRDADTRGQALTASLESGYPLALSERWT-----LEPQAQLIYQHTRV 734

Query: 571 GKFSRSENHVNLLGSRQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFVEMDG 630
      FSD+ + V + L R+G + + +++ + P+AA+N F G
Sbjct: 735 DDFSDAV-SEVRIRDDNALTARLGARLQGEYAAAAQV-WRPYAALN-----FWRTFSG 785

Query: 631 ERRVI-----NNKTAIESQLGVAVKIKSHLTLQATFNRTGKHHQAKQGA---LNL 678
      E V+ T++E G +V + L L T Q +GA L +
Sbjct: 786 ENTVVLGEDSIDTRRGATSLELAAGASVTLARSLALYGRLAYATSIDSQYLRGASAQLGM 845

Query: 679 QWTF 682
      ++T+
Sbjct: 846 RYTW 849

```

tr Q883X2 Autotransporter, putative [PSPT02225] [*Pseudomonas syringae* 773
 (pv. AA
 tomato)] align

Score = 63.9 bits (154), Expect = 9e-09
 Identities = 69/283 (24%), Positives = 116/283 (40%), Gaps = 39/283 (13%)

```

Query: 407 RKGLWLRVIDGHSNQWVQGKTAPVEGYRK---GVQLGGEVFTWQNESNQLSIGLMGGQAE 463
      + G W+R N A GY++ G LG + + L+ G+M GQ+
Sbjct: 508 QSGAWMRTYGNKFNV---SDASGFGYQQTQQGFSLGADGKVPMDGQWLA-GVMACQSS 562

Query: 464 QRSTFHNPDNDLTGNNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQFRH--RINTED 521
      + D +G V + G Y+TW D TG Y D +++ RF + R+N D
Sbjct: 563 SDSL-----DRGASGKVDSYYVGAYSTW---LSDTGYFFDGVLFKFNRFNNKARVNLSD 614

Query: 522 GTER---FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDSEN 578
      GT +++ G+ AS+E G + L + +++P +QL + V GK + +N
Sbjct: 615 GTRTKGDYSNSGVGASLEFGRHIKLDNGY-----FVEPYSQLAGVVVEGKDYELDN 665

Query: 579 ---AHVNLLGSRQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFVEMDGERRVI 635
      A +L +R L ++G F L + ++P+ A H E+ V
Sbjct: 666 GMRAENDL--TRSLVGKLGATTGRNFDLQGRTVQPYVR-TAWVHEFAKNNEVQVNDNVF 722

Query: 636 NNK---TAIESQLGVAVKIKSHLTLQATFNRTGKHHQAKQGA 675
      NN + E +G+A + + A F G + GA
Sbjct: 723 NNDLSGSRGELGIGIAASLSERFQVHADFEHSNGDKVEQPWGA 765

```

tr Q7WIB0 Putative autotransporter [BB2941] [*Bordetella bronchiseptica* 937 AA
 (Alcaligenes bronchisepticus)] align

Score = 55.5 bits (132), Expect = 3e-06
 Identities = 106/493 (21%), Positives = 170/493 (33%), Gaps = 76/493 (15%)

```

Query: 224 IEVTDNSHVIGQTISLDEFRL-ENSLWEPRWDSNVGKLKTT-NADIRFNTKSE---SLLV 278
      ++V D + G T SLD L W S+VG+L A + F + L
Sbjct: 477 LDVADGAQWHGATQSLDRLALGAGGQWRMSAASSVGELSMEPGAADVFGDAAGPGFQTLT 536

```

```

Query: 279 KEDYAGGARFRFAYDPKEAKNTALIFEKNVTGTSDIIFENPIDDLKSLDGHQIIKVNNGTA 338
          AG  F  D          L+  G  +  P  S  Q  +  V  A
Sbjct: 537 VRTLAGAGSFEMRADAALAHADQLVVTDQAEGRHRVWLRAPAGAEPska--QAVLVRAPA 594

Query: 339 D-KHAFRLSGKHQK---GIYTLSSLQQRPEGFLPKCKNAM-----IWR 376
          D K +F L G  +  G Y  L Q+P G  +          +W
Sbjct: 595 DGKASFELDGSDGRADFGTYRYGLAQPPGAWGLVRTGYSSTAAAALDTGGLGAVQGLWY 654

Query: 377 FMHNRLKPPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGTAPVEGYRKG 436
          N L  +  LRLN  + R  ++  R+  + QG +  G
Sbjct: 655 AESNALGKRMG--ELRLNPDAGGAWGRAFSQRQ---RISPRAGRHFQQGVS-----G 701

Query: 437 VQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTGNNVKGFGAGVYATWHQLQ 496
          ++LG +  W  +  G + G  F  +  + +V G+  + A
Sbjct: 702 IELGADR-AWPVAGGRWHAGGLLGYTRASRGFSGQKGHTDSVHVGGYATYIGAN----- 755

Query: 497 DKQTGAYADSWMQYQFRHRINTEDGTER-----FTSKGITASIEAGYNALLAEHFTKKG 551
          G YAD+ ++  RF +  +  R  +  + G+  ++EAG  L  H+
Sbjct: 756 ----GVYADATLRASRFENSFDVPGWAGRTVSGSYRANGVGVTLGARRLALDRHW---- 807

Query: 552 NSLRVYLQPPAQLTYLGVNG-KFSDSENAHVNLLGSRQLQTRVGVAQAQFSLYKNIAIE 610
          +++PQA+L +  G  ++ S  +  G  LQ RVG QA  +F L  ++
Sbjct: 808 -----FVEPQAELAWFRAGGGTYTASNGLRIEDDGGTSLQARVGAQAGRRFDLGGAVVQ 862

Query: 611 PFAAVNALYHNKPFPG-VEMDG-ERRVINNKTAIESQLGVAVKIKSHLTLQATFNRQTGKH 668
          P+A ++ +  K  V  +G  R  +E  LGVA  +  L  A++  G
Sbjct: 863 PYAQLSWVQELKGVSTVRTNGIAHRTDLGAGRVELGLGVAAALGKGHNLYASYEYAHGPR 922

Query: 669 HQAKQGALNLQWT 681
          L+L WT
Sbjct: 923 -----LSLPWT 928

```

tr Q7W6E1 Putative autotransporter [BPP2975] [Bordetella parapertussis] 937 AA

align

Score = 55.5 bits (132), Expect = 3e-06

Identities = 106/493 (21%), Positives = 170/493 (33%), Gaps = 76/493 (15%)

```

Query: 224 IEVTDNSHVIGQTISLDEFRL-ENSLWEPRWDSNVGKLKTT-NADIRFNTKSE---SLLV 278
          ++V D +  G T SLD  L  W  S+VG+L  A + F  +  L
Sbjct: 477 LDVADGAQWHGATQSLDRLALGAGGQWRMSAASSVGELSMEPGAADVFGDAAGPGFQTLT 536

Query: 279 KEDYAGGARFRFAYDPKEAKNTALIFEKNVTGTSDIIFENPIDDLKSLDGHQIIKVNNGTA 338
          AG  F  D          L+  G  +  P  S  Q  +  V  A
Sbjct: 537 VRTLAGAGSFEMRADAALAHADQLVVTDQAEGRHRVWLRAPAGAEPska--QAVLVRAPA 594

Query: 339 D-KHAFRLSGKHQK---GIYTLSSLQQRPEGFLPKCKNAM-----IWR 376
          D K +F L G  +  G Y  L Q+P G  +          +W
Sbjct: 595 DGKASFELDGSDGRADFGTYRYGLAQPPGAWGLVRTGYSSTAAAALDTGGLGAVQGLWY 654

Query: 377 FMHNRLKPPPIPYCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGTAPVEGYRKG 436
          N L  +  LRLN  + R  ++  R+  + QG +  G
Sbjct: 655 AESNALGKRMG--ELRLNPDAGGAWGRAFSQRQ---RISPRAGRHFQQGVS-----G 701

```

Query: 437 VQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDNDLTTGNVKGFGAGVYATWHQLQ 496
 ++LG + W + G + G F + + +V G+ + A
 Sbjct: 702 IELGADR-AWPVAGGRWHAGLLGYTRASRGFSGQGKHTDSVHVGGYATYIGAN----- 755

Query: 497 DKQTGAYADSWMQYQRFRRHINTEDGTER-----FTSKGITASIEAGYNALLAEHFTKKG 551
 G YAD+ ++ RF + + R + + G+ ++EAG L H+
 Sbjct: 756 ----GVYADATLRASRFENSFDVPGWAGRTVSGSYRANGVGVTLAARRLALDRHW---- 807

Query: 552 NSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLLGSRQLQTRVGVQAKAQFSLYKNIAIE 610
 +++PQA+L + G ++ S + G LQ RVG QA +F L ++
 Sbjct: 808 -----FVEPQAEALAWFRAGGGTYTASNGLRIEDDGGTSLQARVGAQAGRRFDLRGGAVVQ 862

Query: 611 PFAAVNALYHNKPPFG-VEMDG-ERRVINNKTAIESQLGVAVKIKSHLTLQATFNRQTGKH 668
 P+A ++ + K V +G R +E LGVA + L A++ G
 Sbjct: 863 PYAQLSWVQELKGVSTVRTNGIAHRTDLGAGRVELGLGVAAALGKGHNLYASYEYAHGPR 922

Query: 669 HQAKQGALNLQWT 681
 L+L WT
 Sbjct: 923 -----LSLPWT 928

tr Q7WQ80 Autotransporter [BB0452] [Bordetella bronchiseptica 2377
 (Alcaligenes AA
 bronchisepticus)] align

Score = 53.9 bits (128), Expect = 1e-05

Identities = 58/257 (22%), Positives = 103/257 (39%), Gaps = 29/257 (11%)

Query: 408 KGLWLRLVIDGHSNQWVQGTAP-VEGYRKGVLGGEVFTWQNESNQL-SIGLMGGQAEQR 465
 +G W R + G+ AP +G+ G QLG +++ + + +G+ GG A R
 Sbjct: 2103 RGGWARTFGRRRFERSAGGEAAPSFDGHLAQAQLGADLYARSSATRHTDAFGVFGGYATVR 2162

Query: 466 STFHN---PDNDLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRRHINTEDG 522
 H + + T ++ G Y T G Y D+ + R+R + +
 Sbjct: 2163 GDVHGLARGEIQAVGTSTLRATQLGAYWT----HTGPGGWYIDTVLAGTRYRQQTSSAQ 2218

Query: 523 TERFTSK-GITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDSENAHV 581
 + G+TAS+EAGY L + R ++PQAQ+ Y + + V
 Sbjct: 2219 VGAVSRGWGMTASVEAGYPWQL-----NPRWRIEPQAQVVYQQLGIANGADRSTV 2269

Query: 582 NLLGSRQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALY-----HNKPPFGVEMDGER 632
 + L R+G + Q++ Y + PF V+ L+ GV +
 Sbjct: 2270 SYKTPDALTRLGTRLGQYA-YGKAQLRPFMGVSLLDHFTGADTVTFAGAHGVRASRQN 2328

Query: 633 RVINNKTAEIESQLGVAV 649
 ++ K +++QLG +V
 Sbjct: 2329 TAVDLKAGVDTQLGKSV 2345

tr Q7WHU5 Autotransporter [BB3111] [Bordetella bronchiseptica 528
 (Alcaligenes AA
 bronchisepticus)] align

Score = 53.5 bits (127), Expect = 1e-05

Identities = 55/220 (25%), Positives = 89/220 (40%), Gaps = 42/220 (19%)

Query: 478 TGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTEDGTER-----FTSKGIT 532
TG G YAT+ + G Y D ++ R+ H D R + + G+
Sbjct: 328 TGEGDSVHVGAATYIE----DGGFYMDGIVRVARYAHEFKAPDAKGRRVRGKYRANGVG 383

Query: 533 ASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLT-YLGVNGKFSDSENAHVNLLGSRQLQT 591
AS+E G + FT G Y++PQ ++ + G + ++ V G L
Sbjct: 384 ASLELG-----KRFTWAG---AWYVEPQLEMAVFHAQGGSYRAGQDLRVKDNGLTSLLG 434

Query: 592 RVGVQAKAQFSLYKNIAIEPFPAVNALYHNKPFVEMDGERRV----INNKTAI-----E 642
RVG+ QF L ++P+A ++ L E DG+ V + +K+ + E
Sbjct: 435 RVGLHVGRQFDLGDGRVVQPYAKLSWLQ-----EFDGKNTVRTNGVRHKSRLDGGRAE 487

Query: 643 SQLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQWTF 682
LGVA ++ H +L G + AK + WTF
Sbjct: 488 LDLGVAAQLGKHGSLY-----GSYEYAKGSRQTMPWTF 520

tr Q7WC76 Autotransporter [BPP0452] [Bordetella 1769 AA
parapertussis] align

Score = 53.5 bits (127), Expect = 1e-05

Identities = 58/257 (22%), Positives = 103/257 (39%), Gaps = 29/257 (11%)

Query: 408 KGLWLRVIDGHSNQWVQKGTAP-VEGYRKGVLGGEVFTWQNESNQL-SIGLMGGQAEQR 465
+G W R + G+ AP +G+ G QLG +++ + + + G+ GG A R
Sbjct: 1495 RGGWARTFGRRFERSAGGEAAPSFDGHLAQAQLGADLYARSSGTRHTDAFGVFGGYATVR 1554

Query: 466 STFHN---PDTDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTEDG 522
H + + T ++ G Y T G Y D+ + R+R + +
Sbjct: 1555 GDVHGLARGEIQAVGTSTLRATQLGAYWT---HTGPGGWYIDTVLAGTRYRQQTKSSAQ 1610

Query: 523 TERFTSK-GITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDSENAHV 581
+ G+TAS+EAGY L + R ++PQAQ+ Y + + V
Sbjct: 1611 VGAVSRGWGMTASVEAGYPWQL-----NPRWRIEPAQVVYQQLGIANGADRVSTV 1661

Query: 582 NLLGSRQLQTRVGVQAKAQFSLYKNIAIEPFPAVNALY-----HNKPFVEMDGER 632
+ L R+G + Q++ Y + PF V+ L+ GV +
Sbjct: 1662 SYKTPDALTLARLGTRLSGQYA-YGKAQLRPFMGVSLLHDFTGADTVTFAGAHGVRASRQN 1720

Query: 633 RVINNKTAIESQLGVAV 649
++ K +++QLG +V
Sbjct: 1721 TAVDLKAGVDTQLGKSV 1737

tr Q8VV95 Vag8 protein (Autotransporter) [vag8-2] [Bordetella pertussis] 915 AA
align

Score = 52.0 bits (123), Expect = 4e-05

Identities = 61/252 (24%), Positives = 100/252 (39%), Gaps = 42/252 (16%)

Query: 436 GVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDNDLTTGNVKGFGAGVYATWHQL 495
G++LG + + S+G++ G +E R D G+V G Y ++ L
Sbjct: 678 GIELGLDRRVAGGATTAWSVGMLAGYSETRR-----DGGAYRAGHVHSAHVGAYVSY--L 730

Query: 496 QDKQTGAYADSWMQYQFRH--RINTED---GTERFTSKGITASIEAGYNALLAEHFTKK 550
D +G+Y D ++Y RFRH I T D + S G+ A + G + +
Sbjct: 731 ND--SGSYVDGVVKNRFRHGFDIRTTDLKRVDKHRSHGLGALLRGRRIDIDGGW--- 785

Query: 551 GNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLLGSRQLQTRVGVQAKAQFSLYKNIAI 609
Y++PQA + + G ++ S V G+ R G +A Q L +
Sbjct: 786 -----YVEPQASVAWFHAGGSRYEASNGLRVRADGAHSWVLRAGAEAGRQMLANGNIV 839

Query: 610 EPFA-----AVNALYHNKPFGEVMDGERRVINNKTAI-ESQLGVAVKIKSHLTLQA 659
EP+A A NA+Y N G R V ++ E+++GV + L A
Sbjct: 840 EPYARLGWAQELGADNAVYTN-----GIRHVTRSRGGFAEARVGVGALLGKRHALYA 891

Query: 660 TFNRQTGKHHQA 671
+ G +A
Sbjct: 892 DYEYAKGARFEA 903

tr 066044 Vag8 [vag-8] [Bordetella pertussis] 915 AA
align

Score = 52.0 bits (123), Expect = 4e-05
Identities = 61/252 (24%), Positives = 100/252 (39%), Gaps = 42/252 (16%)

Query: 436 GVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTTGNVKGFGAGVYATWHQL 495
G++LG + + S+G++ G +E R D G+V G Y ++ L
Sbjct: 678 GIELGLDRRVAGGATTAWSVGMLAGYSETRR-----DGGAYRAGHVHSAHVGAIVSY--L 730

Query: 496 QDKQTGAYADSWMQYQFRH--RINTED---GTERFTSKGITASIEAGYNALLAEHFTKK 550
D +G+Y D ++Y RFRH I T D + S G+ A + G + +
Sbjct: 731 ND--SGSYVDGVVKNRFRHGFDIRTTDLKRVDKHRSHGLGALLRGRRIDIDGGW--- 785

Query: 551 GNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLLGSRQLQTRVGVQAKAQFSLYKNIAI 609
Y++PQA + + G ++ S V G+ R G +A Q L +
Sbjct: 786 -----YVEPQASVAWFHAGGSRYEASNGLRVRADGAHSWVLRAGAEAGRQMLANGNIV 839

Query: 610 EPFA-----AVNALYHNKPFGEVMDGERRVINNKTAI-ESQLGVAVKIKSHLTLQA 659
EP+A A NA+Y N G R V ++ E+++GV + L A
Sbjct: 840 EPYARLGWAQELGADNAVYTN-----GIRHVTRSRGGFAEARVGVGALLGKRHALYA 891

Query: 660 TFNRQTGKHHQA 671
+ G +A
Sbjct: 892 DYEYAKGARFEA 903

tr Q7WQ83 Autotransporter [BB0450] [Bordetella bronchiseptica] 2152
(Alcaligenes AA
bronchisepticus)] align

Score = 51.6 bits (122), Expect = 5e-05
Identities = 47/220 (21%), Positives = 88/220 (39%), Gaps = 23/220 (10%)

Query: 407 RKGLWLRLVIDGHSNQWVQKTAP-VEGYRKGVQLGGEVFTWQNESNQLSI-GLMGGQAEQ 464
R+G W R + G P +G+ G+Q G +++ + + + G+ GG A
Sbjct: 1876 RRGAWTRAFAFGRTFERSGSGDVPDFDGHVAGLQAGVDLYARRSDQGHADLAGVFGGYANA 1935

Query: 465 RSTFHNPDNDLTTGNVKGFGA-----GVYATWHQLQDKQTGAYADSWMQYQRFHRI-N 518
 R D G + Y + +G Y D+ + R+ + +
 Sbjct: 1936 RGHM-----DGFARGETGAYAGKPDNLNAYYIGGYWTHIGPSGWYVDAVLGTRYEQKAKS 1990

Query: 519 TEDGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDSEN 578
 + D G+TAS+EAGY + E + +++PQAQL Y + + +
 Sbjct: 1991 SNDLRTEAKGWGTASVEAGYPVPIGEKW-----HIEPQAQLVYQRLTVSNGEDDV 2041

Query: 579 AHVNLLGSRQLQTRVGQAKAQFSLYKNIAIEPFPAVNAL 618
 + V+ + R+G + Q++ Y + PF V+ L
 Sbjct: 2042 SSVSYRTPDSVTARLGARLSGQYA-YNTTQLRPFMEVSL 2080

tr Q7WC79 **Autotransporter [BPP0449] [Bordetella** 1616 AA
parapertussis] align

Score = 51.6 bits (122), Expect = 5e-05
 Identities = 47/220 (21%), Positives = 88/220 (39%), Gaps = 23/220 (10%)

Query: 407 RKGLWLRVIDGHSNQWVQKTAP-VEGYRKGVLGGEVFTWQNESNQLSI-GLMGGQAEQ 464
 R+G W R + G P +G+ G+Q G +++ +++ + G+ GG A
 Sbjct: 1340 RRGAWTRAFGRTFERSGSGDVPFRFDGHVAGLQAGVDLYARRSDQGHADLAGVFGGYANA 1399

Query: 465 RSTFHNPDNDLTTGNVKGFGA-----GVYATWHQLQDKQTGAYADSWMQYQRFHRI-N 518
 R D G + Y + +G Y D+ + R+ + +
 Sbjct: 1400 RGHM-----DGFARGETGAYAGKPDNLNAYYIGGYWTHIGPSGWYVDAVLGTRYEQKAKS 1454

Query: 519 TEDGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDSEN 578
 + D G+TAS+EAGY + E + +++PQAQL Y + + +
 Sbjct: 1455 SNDLRTEAKGWGTASVEAGYPVPIGEKW-----HIEPQAQLVYQRLTVSNGEDDV 1505

Query: 579 AHVNLLGSRQLQTRVGQAKAQFSLYKNIAIEPFPAVNAL 618
 + V+ + R+G + Q++ Y + PF V+ L
 Sbjct: 1506 SSVSYRTPDSVTARLGARLSGQYA-YNTTQLRPFMEVSL 1544

tr Q7W9Y1 **Autotransporter [BPP1618] [Bordetella parapertussis]** 519 AA
align

Score = 51.6 bits (122), Expect = 5e-05
 Identities = 57/243 (23%), Positives = 92/243 (37%), Gaps = 47/243 (19%)

Query: 455 IGLMGGQAEQRSTFHNPDNDLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRF 514
 +G + G R F D TG+ G YAT+ + G Y D ++ R R
 Sbjct: 301 VGAVAGYTNGRIKF-----DRGGTGDDDSVHVGAATYIE----DGGFYMDGIVRVSRIR 351

Query: 515 HRINTEDGTER-----FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV 569
 H +D R + G+ AS+E G + FT G Y++PQ ++
 Sbjct: 352 HAFKVDDAKGRRVRGQYRGNGVGASLELG-----KRFTWPG---AWYVEPQLEVAAFRA 402

Query: 570 NG-KFSDSENAHVNLLGSRQLQTRVGQAKAQFSLYKNIAIEPFPAVNALYHNKPFVEM 628
 G ++ S + G+ + R+G+ QF L ++P+ ++ + E
 Sbjct: 403 QGADYTASNGLRIKDDGTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ-----EF 455

Query: 629 DGERRVINNKT-----AIESQLGVAVKIKSHLTLQATFNROTGKHHQAKQGALNLQ 679
 DG+ V N E LGVA ++ H +L G + AK +
 Sbjct: 456 DGKGTVRTNGVRHKNRLDGGRAELDLGVAAQLGKHGSLY-----GSYEYAKGSRQTMP 508

Query: 680 WTF 682
 WTF
 Sbjct: 509 WTF 511

tr Q9F290 **YapC protein (Putative autotransporter) (Putative autotransporter protein) [yapC] [Yersinia pestis]** 638
 align

Score = 51.2 bits (121), Expect = 6e-05
 Identities = 39/205 (19%), Positives = 90/205 (43%), Gaps = 22/205 (10%)

Query: 409 GLWLRVIDGHSNQWVQGKTAPVEGYRKGVLGGEVFTWQNESNQLSIGLMGGQAEQRSTF 468
 G+W R + S + K + G++G + N N L + +
 Sbjct: 382 GVWARYLTDDS-RLSDNKNI AFKNTLSGMEIGADKQLGLNRGNMLIGAFTSYSSSDVKST 440

Query: 469 HNPDTDNLTGTVKGFAGVYATWHQLQDKQTGAYADSWMQYQRFHRINTEDGTERFTS 528
 H+ + G+++ +G G+Y T+ Q+G Y D+ ++ RF +++NT++ +
 Sbjct: 441 HDAN-----GDIRSYGGGLYLTLYLD---QSGFYVDTVLKANRFNNKMNTQETRGEYNQ 490

Query: 529 KGITASIEAGYNALLAEHFTKKGNLSRVYLQPQAQLTYLGV-NGKFSDSENAHVNLGSR 587
 +T S+E+GY + + + L+P +++Y + + ++ S + +
 Sbjct: 491 NALTTSVESGYQWPVYAN-----LVLEPYGKVSYSRIGSADYTLNMGVAEVAKAD 541

Query: 588 QLQTRVGQAKAQFSLYKNIAIEPF 612
 +Q +G A +S+ + I+P+
 Sbjct: 542 SVQGE LGTVLAASYSI-NQMTIKPY 565

tr Q88ID0 **Outer membrane autotransporter [PP3069] [Pseudomonas putida (strain KT2440)]** 825
 align

Score = 50.8 bits (120), Expect = 8e-05
 Identities = 57/222 (25%), Positives = 97/222 (43%), Gaps = 36/222 (16%)

Query: 477 TTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFHRINTEDG-TERFTSKGITASI 535
 + G++K G V W + + GAY D+ +QY R R +E G T TAS+
 Sbjct: 624 SVGDLKLDGDSVGTYWTLVGPPQ--GAYLDAVLQYTRLDGRARSERGDTLNLGDHAWTASL 681

Query: 536 EAGYNALLAEHFTKKGNLSRVYLQPQAQLTYLGVNGKFSDSENAHVNLGSRQLQTRVGV 595
 E+GY L+E R ++PQAQL V + + + ++ +L R+G+
 Sbjct: 682 ESGYPITLSE-----RWRVEPQAQLIAQKVALESARDSVSRISHDAQVELTGRLGL 732

Query: 596 QAKAQFSLYKNIAIEPFPAVNALYHNKPFGEVDGERRVIN-----NKTAIESQ 644
 + + F+ ++PFA VN L+H DG R + T+++ +
 Sbjct: 733 RLEGFTGSSGRLLQPFAQVN-LWHG-----DGGRDTLTFFDADKIKTDYRYTSVQLE 784

Query: 645 LGVAVKIKSHLTL---QATFNROTGKHHQAKQGALNLQWTF 682
 GV ++ L+L Q T N + + +A L ++W F
 Sbjct: 785 SGVVAQVNEALSLHGGVQYTANLDS-RQQEASGVNLGVRWQF 825

sp P76017 **Hypothetical protein ycgV [ycgV] [Escherichia** 955 AA
YCGV_ECOLI **coli]** align

Score = 50.1 bits (118), Expect = 1e-04

Identities = 58/218 (26%), Positives = 94/218 (42%), Gaps = 32/218 (14%)

Query: 410 LWLRVIDGHSNQWVQGKTAPVEGYRKGVLGGEVFTWQNESNQLSIGLMGGQAEQRSTFH 469
+WLR G + + GK + + G+Q GG+ ++ L +GL G ST

Sbjct: 694 IWLRSYGGSLDSFASGKLSGFDMGYSIGQFGGD--KRLSDVMPLYVGLYIG-----STHA 746

Query: 470 NPDTDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRRHINTEDG-----TE 524
+PD G + G+YA++ Q G Y+D ++ R ++ + D

Sbjct: 747 SPDYSG-GDGTARSDYMGMYASYM----AQNGFYSDLVIKASRQKNSFHVLD SQNNGVNA 801

Query: 525 RFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNG---KFSDSENAHV 581
T+ G++ S+EAG + F Y++PQ QLTY N K S+ N H+

Sbjct: 802 NGTANGMSISLEAG-----QRFNLSPTGYGFYIEPQTQLTYSHQNEMTMKASNGLNIHL 855

Query: 582 N----LLGSRQLQTRVGVA-KAQFSLY-KNIAIEPFA 613
N LLG + + A +Q ++Y K AI F+

Sbjct: 856 NHYESLLGRASMILGYDITAGNSQLNVYVKTGAIREFS 893

tr Q881W9 **Autotransporter, putative [PSPT02763] [Pseudomonas syringae** 927
(pv. **tomato)]** AA
align

Score = 49.7 bits (117), Expect = 2e-04

Identities = 69/290 (23%), Positives = 112/290 (37%), Gaps = 39/290 (13%)

Query: 411 WLRVIDGHSNQWVQGKTAP-VEGYRKGVLGGEVFTWQNESNQ-LSIGLMGGQAEQ---- 464
W RV Q G +P ++ KG Q+G +V+ W + Q L IGL Q

Sbjct: 657 WARVFGSDFKQWQSGTVSPGLDASLKGQIGHDVYAWSLDGQQILRIGLFVAQNRLDGKV 716

Query: 465 ---RSTFHNPDTDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRRHINTED 521
FH TG +K G V A W T +Y D+ + R ++

Sbjct: 717 QGFAGGFHARH-----TGRIKLHGDSVGAYW--TLSSPTASYVDALVMSTRLDGYSRSDR 769

Query: 522 GTERFTSKG--ITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDSENA 579
G R ++G ++ S+EAG+ +L R +PQ Q+ + ++ +

Sbjct: 770 GL-RIDTQGHALSLSVEAGHPFVLTP-----RWVAEPQVQIIHQRIDLDDQHDGIS 819

Query: 580 HVNLLGSRQLQTRVGVAKAQFSLYKNIAIEPFAAVNALYHNK--PFGVEMDGERRVINN 637
HV R+G++ K +++L + IEP+ N L+ N V D R+

Sbjct: 820 HVGFDSPYNTGRLGIRFKGRYAL-AGMPIEPYLRAN-LWRNAGGHDTVTFDHTERIKTA 877

Query: 638 KTAIESQLGVAVKIK----SHLTLQATFNRTGKHHQAKQGA---LNLQW 680
+ LG + IK + + A +NR H + A + L W

Sbjct: 878 HRSTTGSLGAGMVIKVASDTSVYWGADYNRDLNSHDSSGANASLGVRLAW 927

tr Q7WL85 Autotransporter [vag8] [*Bordetella bronchiseptica* (*Alcaligenes bronchisepticus*)]

align

Score = 49.7 bits (117), Expect = 2e-04

Identities = 59/252 (23%), Positives = 100/252 (39%), Gaps = 42/252 (16%)

Query: 436 GVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTGTVKGFAGVYATWHQL 495
G++LG + + S+G++ G +E R D G+V G Y ++ L
Sbjct: 678 GIELGIDRRVAGGATTAWSVGMLAGYSETRR-----DGGAYRAGHVHSAHVGAYVSY--L 730

Query: 496 QDKQTGAYADSWMQYQFRH--RINTED---GTERFTSKGITASIEAGYNALLAEHFTKK 550
D +G+Y D ++Y RFRH + T D + S G+ A + G + +
Sbjct: 731 ND--SGSYVDGVVKYNRFRHGFVDVRTTDLKRVDKHRSHGLGALLRGRRIDIDGGW--- 785

Query: 551 GNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLLGSRQLQTRVGVQAKAQFSLYKNIAI 609
Y++PQA + + +G ++ S V + R G +A Q L +
Sbjct: 786 -----YVEPQASVAWFHADGSRYEASNGLRVRADSAHSWVLRAGAEAGRQMRLANGNIV 839

Query: 610 EPFA-----AVNALYHNKPFGVEMDGERRVINNKTAI-ESQLGVAVKIKSHLTLQA 659
EP+A A NA+Y N G R V ++ E+++GV + L A
Sbjct: 840 EPYARLGWAQELGADNAVYTN-----GIRHVTRSRGGFAEARVGVGALLGKRHALYA 891

Query: 660 TFNRQTGKHHQA 671
+ G +A
Sbjct: 892 DYEYAKGARFEA 903

tr Q7W7U5 Autotransporter [vag8] [*Bordetella parapertussis*] 915 AA
align

Score = 49.7 bits (117), Expect = 2e-04

Identities = 59/252 (23%), Positives = 100/252 (39%), Gaps = 42/252 (16%)

Query: 436 GVQLGGEVFTWQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTGTVKGFAGVYATWHQL 495
G++LG + + S+G++ G +E R D G+V G Y ++ L
Sbjct: 678 GIELGIDRRVAGGATTAWSVGMLAGYSETRR-----DGGAYRAGHVHSAHVGAYVSY--L 730

Query: 496 QDKQTGAYADSWMQYQFRH--RINTED---GTERFTSKGITASIEAGYNALLAEHFTKK 550
D +G+Y D ++Y RFRH + T D + S G+ A + G + +
Sbjct: 731 ND--SGSYVDGVVKYNRFRHGFVDVRTTDLKRVDKHRSHGLGALLRGRRIDIDGGW--- 785

Query: 551 GNSLRVYLQPQAQLTYLGVNG-KFSDSENAHVNLLGSRQLQTRVGVQAKAQFSLYKNIAI 609
Y++PQA + + +G ++ S V + R G +A Q L +
Sbjct: 786 -----YVEPQASVAWFHADGSRYEASNGLRVRADSAHSWVLRAGAEAGRQMRLANGNIV 839

Query: 610 EPFA-----AVNALYHNKPFGVEMDGERRVINNKTAI-ESQLGVAVKIKSHLTLQA 659
EP+A A NA+Y N G R V ++ E+++GV + L A
Sbjct: 840 EPYARLGWAQELGADNAVYTN-----GIRHVTRSRGGFAEARVGVGALLGKRHALYA 891

Query: 660 TFNRQTGKHHQA 671
+ G +A
Sbjct: 892 DYEYAKGARFEA 903

tr Q7WHU6 **Autotransporter [BB3110] [Bordetella bronchiseptica** 770
(**Alcaligenes** AA
bronchisepticus] align

Score = 49.3 bits (116), Expect = 2e-04

Identities = 57/243 (23%), Positives = 95/243 (38%), Gaps = 47/243 (19%)

Query: 455 IGLMGGQAEQRSTFHNPDNDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFR 514
+G + G R F D TG+ G YAT+ + G Y D ++ R R
Sbjct: 552 VGAVAGYTNRIKF-----DRGGTGDDDSVHVGAAYATYIE----DGGFYMDGIVRVSRIR 602

Query: 515 HRINTEDGTER-----FTSKGITASIEAGYNALLAEHFTKKGNLSRVYLQPQAQLTYLGV 569
H +D R + G+ AS+E G + FT G Y++PQ ++
Sbjct: 603 HAFKVDDAKGRRVRGQYRGNGVGASLELG-----KRFTWPG---AWYVEPQLEVAAFHA 653

Query: 570 NG-KFSDSENAHVNLGSRQLQTRVGVQAKAQFSLYKNIAIEPFPAAVNALYHNKPFGVEM 628
G ++ S + G+ + R+G+ QF L ++P+ ++ + E
Sbjct: 654 QGADYTASNGLRIKDDGTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ-----EF 706

Query: 629 DGERRV----INNKTAI-----ESQLGVAVKIKSHLTLQATFNROTGKHHQAKQGALNLQ 679
DG+ V I +K + E +GVA ++ H +L G + AK +
Sbjct: 707 DGKGTVRTNDRHKVRLDGGRAELAVGVASQLGKHGSL-----FGSYEYAKGSRQTMP 759

Query: 680 WTF 682

WTF

Sbjct: 760 WTF 762

tr O86135 **Tracheal colonization factor precursor [tcfA2] [Bordetella** 647 AA
pertussis] align

Score = 49.3 bits (116), Expect = 2e-04

Identities = 57/243 (23%), Positives = 95/243 (38%), Gaps = 47/243 (19%)

Query: 455 IGLMGGQAEQRSTFHNPDNDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFR 514
+G + G R F D TG+ G YAT+ + G Y D ++ R R
Sbjct: 429 VGAVAGYTNRIKF-----DRGGTGDDDSVHVGAAYATYIE----DGGFYMDGIVRVSRIR 479

Query: 515 HRINTEDGTER-----FTSKGITASIEAGYNALLAEHFTKKGNLSRVYLQPQAQLTYLGV 569
H +D R + G+ AS+E G + FT G Y++PQ ++
Sbjct: 480 HAFKVDDAKGRRVRGQYRGNGVGASLELG-----KRFTWPG---AWYVEPQLEVAAFHA 530

Query: 570 NG-KFSDSENAHVNLGSRQLQTRVGVQAKAQFSLYKNIAIEPFPAAVNALYHNKPFGVEM 628
G ++ S + G+ + R+G+ QF L ++P+ ++ + E
Sbjct: 531 QGADYTASNGLRIKDDGTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ-----EF 583

Query: 629 DGERRV----INNKTAI-----ESQLGVAVKIKSHLTLQATFNROTGKHHQAKQGALNLQ 679
DG+ V I +K + E +GVA ++ H +L G + AK +
Sbjct: 584 DGKGTVRTNDRHKVRLDGGRTTELAVGVASQLGKHGSL-----FGSYEYAKGSRQTMP 636

Query: 680 WTF 682

WTF

Sbjct: 637 WTF 639

Score = 49.3 bits (116), Expect = 2e-04

Identities = 57/243 (23%), Positives = 95/243 (38%), Gaps = 47/243 (19%)

Query: 455 IGLMGGQAEQRSTFHNPDNDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFR 514
+G + G R F D TG+ G YAT+ + G Y D ++ R R

Sbjct: 429 VGAVAGYTNGRIKF-----DRGGTGDDDSVHVGAYATYIE----DGGFYMDGIVRVSRIR 479

Query: 515 HRINTEDGTER-----FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV 569
H +D R + G+ AS+E G + FT G Y++PQ ++

Sbjct: 480 HAFKVDDAKGRRVRGQYRGNGVGASLELG-----KRFTWPG---AWYVEPQLEVAAFHA 530

Query: 570 NG-KFSDSENAHVNNLLGSRQLQTRVGVOAKAQFSLYKNIAIEPFPAVNALYHNKPFGVEM 628
G ++ S + G+ + R+G+ QF L ++P+ ++ + E

Sbjct: 531 QGADYTASNGLRIKDDGTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ-----EF 583

Query: 629 DGERRV----INNKTAI-----ESQLGVAVKIKSHLTLQATFNRTGKHHQAKQGALNLQ 679
DG+ V I +K + E +GVA ++ H +L G + AK +

Sbjct: 584 DGKGTVRTNDIRHKVRLDGGRTTELAVGVASQLGKHGSL-----FGSYEYAKGSRQTMP 636

Query: 680 WTF 682

WTF

Sbjct: 637 WTF 639

tr Q9F4B3 BapB protein [bapB] [Bordetella pertussis] 482 AA
align

Score = 49.3 bits (116), Expect = 2e-04

Identities = 57/243 (23%), Positives = 95/243 (38%), Gaps = 47/243 (19%)

Query: 455 IGLMGGQAEQRSTFHNPDNDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFR 514
+G + G R F D TG+ G YAT+ + G Y D ++ R R

Sbjct: 264 VGAVAGYTNGRIKF-----DRGGTGDDDSVHVGAYATYIE----DGGFYMDGIVRVSRIR 314

Query: 515 HRINTEDGTER-----FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV 569
H +D R + G+ AS+E G + FT G Y++PQ ++

Sbjct: 315 HAFKVDDAKGRRVRGQYRGNGVGASLELG-----KRFTWPG---AWYVEPQLEVAAFHA 365

Query: 570 NG-KFSDSENAHVNNLLGSRQLQTRVGVOAKAQFSLYKNIAIEPFPAVNALYHNKPFGVEM 628
G ++ S + G+ + R+G+ QF L ++P+ ++ + E

Sbjct: 366 QGADYTASNGLRIKDDGTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ-----EF 418

Query: 629 DGERRV----INNKTAI-----ESQLGVAVKIKSHLTLQATFNRTGKHHQAKQGALNLQ 679
DG+ V I +K + E +GVA ++ H +L G + AK +

Sbjct: 419 DGKGTVRTNDIRHKVRLDGGRTTELAVGVASQLGKHGSL-----FGSYEYAKGSRQTMP 471

Query: 680 WTF 682

WTF

Sbjct: 472 WTF 474

tr Q8GB90 Tracheal colonization factor [tcfA] [Bordetella pertussis] 647 AA

align

Score = 49.3 bits (116), Expect = 2e-04

Identities = 57/243 (23%), Positives = 95/243 (38%), Gaps = 47/243 (19%)

Query: 455 IGLMGQAQAEQRSTFHNPD TDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRF 514
+G + G R F D TG+ G YAT+ + G Y D ++ R R
Sbjct: 429 VGAVAGYTNGRIKF-----DRGGTGDDDSVHV GAYATYIE----DGGFYMDGIVRVSRIR 479

Query: 515 HRINTEDGTER-----FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV 569
H +D R + G+ AS+E G + FT G Y++PQ ++
Sbjct: 480 HAFKVDDAKGRRVRGQYRGNGVGASLELG-----KRFTWPG---AWYVEPQLEVA AFHA 530

Query: 570 NG-KFSDSENAHV NLLGSRQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFVEM 628
G ++ S + G+ + R+G+ QF L ++P+ ++ + E
Sbjct: 531 QGADYTASNGLRIKDDGTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ-----EF 583

Query: 629 DGERRV----INNKTAI-----ESQLGVAVKIKSHLTLQATFNRTGKHHQAKQGALNLQ 679
DG+ V I +K + E +GVA ++ H +L G + AK +
Sbjct: 584 DGKGTVRTNDIRHKVRLDGGRTTELAVGVASQLGKHGSL-----FGSYEYAKGSRQTMP 636

Query: 680 WTF 682
WTF
Sbjct: 637 WTF 639

tr Q45343 Tracheal colonization factor [tcfA] [Bordetella pertussis] 672 AAalign

Score = 49.3 bits (116), Expect = 2e-04

Identities = 57/243 (23%), Positives = 95/243 (38%), Gaps = 47/243 (19%)

Query: 455 IGLMGQAQAEQRSTFHNPD TDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRF 514
+G + G R F D TG+ G YAT+ + G Y D ++ R R
Sbjct: 454 VGAVAGYTNGRIKF-----DRGGTGDDDSVHV GAYATYIE----DGGFYMDGIVRVSRIR 504

Query: 515 HRINTEDGTER-----FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV 569
H +D R + G+ AS+E G + FT G Y++PQ ++
Sbjct: 505 HAFKVDDAKGRRVRGQYRGNGVGASLELG-----KRFTWPG---AWYVEPQLEVA AFHA 555

Query: 570 NG-KFSDSENAHV NLLGSRQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFVEM 628
G ++ S + G+ + R+G+ QF L ++P+ ++ + E
Sbjct: 556 QGADYTASNGLRIKDDGTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ-----EF 608

Query: 629 DGERRV----INNKTAI-----ESQLGVAVKIKSHLTLQATFNRTGKHHQAKQGALNLQ 679
DG+ V I +K + E +GVA ++ H +L G + AK +
Sbjct: 609 DGKGTVRTNDIRHKVRLDGGRTTELAVGVASQLGKHGSL-----FGSYEYAKGSRQTMP 661

Query: 680 WTF 682
WTF
Sbjct: 662 WTF 664

tr Q6U948 **Tracheal colonization factor protein [tcfA] [Bordetella pertussis]** 642 AA align

Score = 49.3 bits (116), Expect = 2e-04

Identities = 57/243 (23%), Positives = 95/243 (38%), Gaps = 47/243 (19%)

Query: 455 IGLMGGQAEQRSTFHNPDNDLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRF 514
+G + G R F D TG+ G YAT+ + G Y D ++ R R
Sbjct: 424 VGAVAGYTNGRIKF-----DRGGTGDDDSVHVGAYATYIE----DGGFYMDGIVRVSRIR 474

Query: 515 HRINTEDGTER-----FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGV 569
H +D R + G+ AS+E G + FT G Y++PQ ++
Sbjct: 475 HAFKVDDAKGRRVRGQYRGNVGASLELG-----KRFTWPG---AWYVEPQLEVAAFHA 525

Query: 570 NG-KFSDSENAHVNLLGSRQLQTRVGVQAKAQFSLYKNIAIEPFPAVNALYHNKPFQVEM 628
G ++ S + G+ + R+G+ QF L ++P+ ++ + E
Sbjct: 526 QGADYTASNGLRIKDDGTNSMLGRLGLHVGRQFDLGDGRVVQPYMKLSWVQ-----EF 578

Query: 629 DGERRV----INNKTAI-----ESQLGVAVKIKSHLTLQATFNRTGKHHQAKQGALNLQ 679
DG+ V I +K + E +GVA ++ H +L G + AK +
Sbjct: 579 DGKGTVRTNDIRHKVRLDGGRTAVGASQLGKHGSL-----FGSYEYAKGSRQTMP 631

Query: 680 WTF 682
WTF
Sbjct: 632 WTF 634

tr Q7WKS2 **Putative autotransporter [bapC] [Bordetella bronchiseptica 993 AA (Alcaligenes bronchisepticus)]** align

Score = 48.1 bits (113), Expect = 5e-04

Identities = 96/486 (19%), Positives = 174/486 (35%), Gaps = 80/486 (16%)

Query: 234 GQTISLDEFRLNSLWEPRWDSNVGKLKTTNADIRFNTKSES-----LLVKEDYAGGAR 287
G T +++ R+E+ W S V L + + T +ES L VK +G
Sbjct: 543 GITNTVNALRIEDGTWTVTGSSAVNSLHLQAGKVAYATPAESDGKFKHLRVKT-LSGSG 601

Query: 288 FRFAYDPKEAKNTALIFEKNVTGTSDIIFENP-----IDDLKSLD-----GHQIIKV 334
F + L+ +G ++ ++ L ++ G +
Sbjct: 602 FEMNASADLSGDLLVVSDEASGQHKVLRGAGTEPTGVESLTLVELPKGSQAGFTLANR 661

Query: 335 NGTADKHAFLRSLGKHQKGIYTLSQLQRPEGFLPKCKN-----AMIWRFMHNRLKPPIP 387
G D AFR G++ L + N + IW N L +
Sbjct: 662 GGVVDAGAFRYRLTPDNGVWGLERTSQLSAVANAALNTGGVGAASSIWAEGNALSKRLG 721

Query: 388 YCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGTAPVEGYRKG VQ--LGGEVFT 445
LRL+ + RT +K + +D + + K V G+ G + G+
Sbjct: 722 --ELRLDPGAGGFWGRTFAQK----QQLDNKAGRRFDQK--VYGFELGADHAIAGQQGR 772

Query: 446 WQNESNQLSIGLMGGQAEQRSTFHNPDNDLTTGNVKGFGAGVYATWHQLQDKQTGAYAD 505
W +G + G R +F + + + ++ + A V G Y D
Sbjct: 773 WH-----VGGLLGYTRARRSFVDDGAGHTDSAHIGAYAAYV-----ADNGFYFD 816

Query: 506 SWMQYQRF RH--RINTEDGTE---RFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQP 560
S ++ RF + + D ++ + G+ A++EAG L + + +++P

Sbjct: 817 STLRSRFFENDFTVTATDAVSIRGKYRANGVGATLEAGKRFTLHDGW-----FVEP 867

Query: 561 QAQLTYLGVNG-KFSDSENAHVNLLGSRQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALY 619
Q++++ +G + + N V G R+G+ A + L K+ I+P+A ++ L

Sbjct: 868 QSEVSLPHASGGTYRAANNLSVKDEGGTSAVLRLGLAAGRRIELGKDRVIQPYATLSWLQ 927

Query: 620 HNKPFGEVMDGERRVINNKTAIESQLGVAVKIKSHLTLOATFNRRQ---TGKHHQAKQGAL 676
E G V N + + LG + + L L A R + AK L

Sbjct: 928 -----EFKGVTTVRTNGYGLRDTDLG-GGRAELALGLAAALGRGHKFYTSYEYAKGNKL 979

Query: 677 NLQWTF 682
L WTF

Sbjct: 980 TLPWTF 985

tr Q83RP3 **Putative adhesion and penetration protein [SF1205] [Shigella flexneri]** 955 AA
align

Score = 47.4 bits (111), Expect = 0.001

Identities = 57/218 (26%), Positives = 93/218 (42%), Gaps = 32/218 (14%)

Query: 410 LWLRVIDGHSNQWVQGKTAPVEGYRKGVLGGEVFTWQNESNQLSIGLMGGQAEQRSTFH 469
+WLR G + + GK + + G+Q GG+ ++ L +GL ST

Sbjct: 694 IWLRSYGGSLSDFASGKLSGFDMGYSIGIQFGGD--KRLSDVMPLYVGLY-----IDSTHA 746

Query: 470 NPDTDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFHRINTEDG-----TE 524
+PD G + G+YA++ Q G Y+D ++ R ++ + D

Sbjct: 747 SPDYSG-GDGTARSDYMGMYASYM----AQNGFYSDLVIKASRQKNSFHVLDSONNGVNA 801

Query: 525 RFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNG---KFSDSENAHV 581
T+ G++ S+EAG + F Y++PQ QLTY N K S+ N H+

Sbjct: 802 NGTANGMSISLEAG-----QRFNLSPTGYGFYIEPQTQLTYSHQNEAMKASNGLNIHL 855

Query: 582 N----LLGSRQLQTRVGVQA-KAQFSLY-KNIAIEPFA 613
N LLG + + A +Q ++Y K AI F+

Sbjct: 856 NHYESLLGRASMILGYDITAGNSQLNVYVKTGAIREFS 893

tr Q7WK68 **Autotransporter [BB2270] [Bordetella bronchiseptica (Alcaligenes bronchisepticus)]** 559 AA
align

Score = 47.4 bits (111), Expect = 0.001

Identities = 50/219 (22%), Positives = 85/219 (37%), Gaps = 42/219 (19%)

Query: 479 GNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFHRINTEDG-----TERFTSKGITA 533
GN G YAT+ G Y D ++ R+ H + T ++ + GI

Sbjct: 360 GNSDSLHVGAAYATYIG---DGGFYLDGIVRVNRYEHDFKADGQRGARVTGKYRANGIGL 415

Query: 534 SIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGK-FSDSENAHVNLLGSRQLQTR 592
S+E G FT G+ +++PQ ++ G ++ S V++ ++ L R

Sbjct: 416 SLETG-----RRFTWAGDW---FVEPQVEVALFRSGGADYTASNGVRVDVASTKSLGR 466

Query: 593 VGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFGEVMDGERRVINNKTA-----IES 643

```
      G+Q   +   L       ++P+A ++ L       E DG  +V  N       E
Sbjct: 467 AGLQVGRKLDLGNKGLVQPYAKLSWLQ-----EFDGVGKVRTNDIGHDVKLRGGRAEL 519

Query: 644 QLGVAVKIKSHLTLQATFNRQTGKHHQAKQGALNLQWTF 682
      LGVA  +   H  +L A++   G       L  + W+F
Sbjct: 520 DLGVAAALGRHSSLFASYEYSKGSR-----LTIPWSF 551
```

tr Q7VVD6 Autotransporter (Pseudogene) [bapC] [Bordetella pertussis] 993 AA

align

Score = 47.4 bits (111), Expect = 0.001

Identities = 93/486 (19%), Positives = 173/486 (35%), Gaps = 80/486 (16%)

```
Query: 234 GQTISLDEFRLNSLWEPRWDSNVGKLKTTNADIRFNTKSES-----LLVKEDYAGGAR 287
      G T +++  R+E+  W       S V L       + + T +ES       L VK  +G
Sbjct: 543 GMTKTVNALRIEDGTWTVTGSSTVNSLHLQAGKVAYATPAESDGEFKHLRVK-TLSGSG 601

Query: 288 FRFAYDPKEAKNTALIFEKNVTGTSDIIFENPIDDLKSLDGHQIIKV----- 334
      F          +   L+   +G  ++       +   ++  +++++
Sbjct: 602 FEMNASADLSGDLLVVSDEASGQHKVLVRGAGTEPTGVESLTLVELPEGSQTKFTLANR 661

Query: 335 NGTADKHAFLRLSGKHQKGIYTLSSLQQRPEGFLPKCKN-----AMIWRFMHNRLKPPIP 387
      G D  AFR       G++ L   +       N       + IW   N L   +
Sbjct: 662 GGVVDAGAFRYRLTPDNGVWGLERTSQLSAVANAALNTGGVGAASSIWYAEGNALSKRLG 721

Query: 388 YCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQKTAPEGYRKG VQ--LGGEVFT 445
      LRL+       + RT  +K   + +D  + +   K   V G+  G   + G+
Sbjct: 722 --ELRLDPGAGGFWRGRTFAQK---QQLDNKAGRRFDQK---VYGFELGADHAIAGQQGR 772

Query: 446 WQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTTGNVKGFGAGVYATWHQLQDKQTGAYAD 505
      W          +G + G   R +F +   +   + ++  + A V       G Y D
Sbjct: 773 WH-----VGGLLGYTRARRSFIDDGAGHTDSAHIGAYAAAYV-----ADNGFYFD 816

Query: 506 SWMQYQRFRRH--RINTEDGTE--RFTSKGITASIEAGYNALLAEHFTKKGNLSLRVYLQP 560
      S ++  RF +   +   D       ++ + G+ A++EAG   L + +       +++P
Sbjct: 817 STLRSARFENDFTVTATDAVSVRGKYRANGVGATLEAGKRFTLHDGW-----FVEP 867

Query: 561 QAQLT-YLGVNGKFSDSENAHVNLLGSRQLQTRVG VQAKAQFSLYKNIAIEPFPAAVNALY 619
      Q++++ +   G +   + N V   G       R+G+ A   + L K+  I+P+A ++ L
Sbjct: 868 QSEVSLFHASGGTYRAANNLSVKDEGGTSAVLRRLGLAAGRRLDGLKDRVIQPYATLSWLQ 927

Query: 620 HNKPFGEVMDGERRVINNKTAIESQLGVAVKIKSHLTLQATFNR---QTGKHHQAKQ GAL 676
      E G   V N   + + L   + +   L L A   R       + AK   L
Sbjct: 928 -----EFKGVTTVRTNGYGLRDTLS-GGRAELALGLAAALGRGHQLYTSYEYAKGNKL 979

Query: 677 NLQWTF 682
      L WTF
Sbjct: 980 TLPWTF 985
```

tr Q7C1Y6 Putative adhesion and penetration protein [S1289] [Shigella flexneri] 955 AA

align

tr O86044 Putative autotransporter (BapC protein) [bapC] [Bordetella 759 AA
pertussis]

align

Score = 47.4 bits (111), Expect = 0.001

Identities = 93/486 (19%), Positives = 173/486 (35%), Gaps = 80/486 (16%)

Query: 234 GQTISLDEFRLNSLWEPRWDSNVGKLKTTNADIRFNTKSES-----LLVKEDYAGGAR 287
G T +++ R+E+ W S V L + + T +ES L VK +G

Sbjct: 309 GMTKTVNALRIEDGTWTVTGSSTVNSLHLQAGKVAYATPAESDGEFKHLRVK-TLSGSGSL 367

Query: 288 FRFAYDPKEAKNTALIFEKNVTGTSDIIFENPIDDLKSLDGHQIIKV----- 334
F + L+ +G ++ + ++ +++++

Sbjct: 368 FEMNASADLSDGDLVVSDEASGQHKVLVRGAGTEPTGVESLTLVELPEGSQTKFTLANR 427

Query: 335 NGTADKHAFLRLSGKHQKGIYTLSSLQQRPEGFLPKCKN-----AMIWRFMHNRLKPPIP 387
G D AFR G++ L + N + IW N L +

Sbjct: 428 GGVVDAGAFRYRLTPDNGVWGLERTSQLSAVANAALNTGGVGAASSIWYAEGNALSKRLG 487

Query: 388 YCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGTAPVEGYRKGVQ--LGGEVFT 445
LRL+ + RT +K + +D + + K V G+ G + G+

Sbjct: 488 --ELRLDPGAGGFWRGRTFAQK---QQLDNKAGRRFDQK---VYGFELGADHAIAGQQGR 538

Query: 446 WQNESNQLSIGLMGGQAEQRSTFHNPDTDNLTTGNVKGFGAGVYATWHQLQDKQTGAYAD 505
W +G + G R +F + + + ++ + A V G Y D

Sbjct: 539 WH-----VGGLGYTRARRSFIDDGAGHTDSAIGAYAAV-----ADNGFYFD 582

Query: 506 SWMQYQRFRRH--RINTEDGTE--RFTSKGITASIEAGYNALLAEHFTKKGNLSRVYLQP 560
S ++ RF + + D ++ + G+ A++EAG L + + +++P

Sbjct: 583 STLRSRPFENDFTVTATDAVSVRGKYRANGVGATLEAGKRFTLHDGW-----FVEP 633

Query: 561 QAQLT-YLGVNGKFSSENHAVNLLGSRQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALY 619
Q++++ + G + + N V G R+G+ A + L K+ I+P+A ++ L

Sbjct: 634 QSEVSLFHASGGTYRAANNLSVKDEGGTSAVLRRLGLAAGRRLDLGKDRVIQPYATLSWLQ 693

Query: 620 HNKPFVEMDGERRVINNKTAIESQLGVAVKIKSHLTLQATFNR---QTGKHQAKQGAL 676
E G V N + + L + + L L A R + AK L

Sbjct: 694 -----EFKGVTTVRTNGYGLRTDLS-GGRAELALGLAALGRGHQLYTSYEYAKGNKL 745

Query: 677 NLQWTF 682

L WTF

Sbjct: 746 TLPWTF 751

tr Q7W8V8 Autotransporter [BPP2022] [Bordetella parapertussis] 538 AA

align

Score = 47.0 bits (110), Expect = 0.001

Identities = 52/220 (23%), Positives = 89/220 (39%), Gaps = 44/220 (20%)

Query: 479 GNVKFGAGVYATWHQLQDKQTGAYADSWMQYQRFRRHINTEDG-----TERFTSKGITA 533
GN G YAT+ G Y D ++ R+ H + T ++ + GI

Sbjct: 339 GNSDSLHVGAYATYIG---DGGFYLDGIVRVNRYEHDFKADGQRGARVTGKYRANGIGL 394

Query: 534 SIEAGYNALLAEHFTKKGNLSRVYLQPQAQLTYLGVNGK--FSDSENAHVNLLGSRQLQT 591

```

      S+E G      FT G+    +++PQ ++ L +GK ++ S    V++ ++ L
Sbjct: 395 SLETG-----RRFTWAGDW---FVEPQVEVA-LFRSGKADYTASNGVRVDVASTKSLLG 444

Query: 592 RVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFQVEMDGERRVINNKA-----IE 642
      R+G+Q    + L      ++P+A ++ L      E DG +V N      E
Sbjct: 445 RLGLQVGRKLDLGNGLVQPYAKLSWLQ-----EFDGVGKVRTNDIGHDVKLGRGRAE 497

Query: 643 SQLGVAVKIKSHLTLQATFNRTGKHHQAKQGALNLQWTF 682
      LGVA + H +L A++ G      L + W+F
Sbjct: 498 LDLGVAAALGKHSSLFASYEYSKGSR-----LTIPWSF 530

```

tr Q7W1F5 **Autotransporter [BPP0735] [Bordetella parapertussis]** 984 AA
align

Score = 46.2 bits (108), Expect = 0.002

Identities = 72/280 (25%), Positives = 110/280 (38%), Gaps = 39/280 (13%)

```

Query: 407 RKGLWLRVIDGHSNQWVQGKTAP-VEGYRKGVLGGEVFTWQNE---SNQLSIGLMGGQA 462
      RK W RVI    Q G P +G    Q G ++    + S++L +    GQA
Sbjct: 711 RKAGWGRVIGQRLTQRWDGDVEPRFKGNIWIAQAGADMLERDRDDGLSDRLGLFSAYGQA 770

Query: 463 EQRSTFHNPDNDLTTGN--VKGFAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTE 520
      + R      G V+ +G G+Y W +L K T Y D+ +    + R ++
Sbjct: 771 DGRVDGFVQGEHGKQAGKLRVEAYGLGLY--WTRL--KHTNWDNVLGMNYYTGRSRSD 826

Query: 521 DGTER-FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDSENA 579
      G      G TAS EAGY+ H      + LQPQAQL Y      +++ +N
Sbjct: 827 RGVAASLEGWGFTASSEAGYS-FFPRH-----DIMLQPQAQLVY-----QYTSLDNT 872

Query: 580 H-----VNLLGSRQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFQVEMDGERRV 634
      H      + G L R+G+ +      + I P+A +N L+H      GE
Sbjct: 873 HDAYSTIRYHGGGALTGRIGLLLQGNADQPER--IRPYARIN-LWHR-----FSHGESVS 924

Query: 635 INNKTAIESQLGVAVKIKSHLTLQATFNRTGKHHQAKQG 674
      +I ++ G + + + L A NRQT + A G
Sbjct: 925 FGPSDSIRTEYG-STSMDLRIGLAAPLNRQTELYASAGY 963

```

tr Q7WP64 **Autotransporter [BB0821] [Bordetella bronchiseptica** 987
(Alcaligenes AA
bronchisepticus)] align

Score = 45.4 bits (106), Expect = 0.003

Identities = 71/275 (25%), Positives = 106/275 (37%), Gaps = 29/275 (10%)

```

Query: 407 RKGLWLRVIDGHSNQWVQGKTAPVEGYRKGVLGGEVFTWQNESNQLS--IGLMG--GQA 462
      RK W RVI    Q G P      + G      ++ + LS +GL G GQA
Sbjct: 714 RKAGWGRVIGQRLTQRWDGDVEPRFKGNIWIAQAGADMLERDRDDGLSDRLGLFGAYGQA 773

Query: 463 EQRSTFHNPDNDLTTGN--VKGFAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTE 520
      + R      G V+ +G G+Y W +L K T Y D+ +    + R ++
Sbjct: 774 DGRVDGFVQGEHGKQAGKLRVEAYGLGLY--WTRL--KHTNWDNVLGMNYYTGRSRSD 829

Query: 521 DGTER-FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDSENA 579

```

```

      G      G TAS EAGY+      H      + LQPQAQL Y      +      +
Sbjct: 830 RGVAASLEGWGF TASSEAGYS-FFPRH-----DIMLQPQAQLVYQYTSLDDTHDAYS 880

Query: 580 HVNLLGSRQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGERRVINNK 639
      +      G      L R+G+      +      +      I P+A +N L+H      GE
Sbjct: 881 TIRYHGGGALTGRIGLLLQGNADQPER--IRPYARIN-LWHR-----FSHGESVSFGPSD 932

Query: 640 AIESQLGVAVKIKSHLTLQATFNRQTGKHHQAKQG 674
      +I ++ G +      +      + L A NRQT + A G
Sbjct: 933 SIRTEYG-STSMDLRIGLAAPLNRTELYASAGYG 966

```

tr Q6G430 **Hypothetical protein [BH05490] [Bartonella henselae** 1291
(Rochalimaea AA
henselae)] align

Score = 44.3 bits (103), Expect = 0.008
Identities = 55/225 (24%), Positives = 91/225 (40%), Gaps = 42/225 (18%)

```

Query: 479 GNVKG---FGAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTEDGTE-----RFTSKG 530
      G V G      + G YAT+      ++G Y DS ++Y ++++ +      + G
Sbjct: 1088 GGVSGINTYSIGAYATYFD----KSGWYLDLSILKYNQYQNNLKAVSTNGIAIEGNYNQWG 1143

Query: 531 ITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNG---KFSDSENAHVNLLGSR 587
      + S EAGY      TK      ++QP AQL++L V G      K S+      +N S
Sbjct: 1144 LGTSFEAGYRF----ETTKSS-----WMQPYAQLSWLQVEGKEIKLSNEMTGDINAFTS- 1193

Query: 588 QLQTRVGVQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGERRVINNKTAIESQL-- 645
      L++ VG+ A +F L ++      +      L N+      D R IN      + L
Sbjct: 1194 -LRSEVGLSAGYEFCLGGDVTSMAYITAAWLREN-----DSNRTTINKLHQFVTDLSG 1246

Query: 646 -----GVAVKIKSHLTLQATFNRQTG-KHHQAKQGALNLQWTF 682
      G++ +      L A      G K Q+ QG L ++++F
Sbjct: 1247 NFGKLGIGLSSLVSKKFKLYAEAQYVKGDVKVQSFQGILGVRYSF 1291

```

tr Q7W7D4 **Putative autotransporter [bapC] [Bordetella parapertussis]** 986 AA
align

Score = 44.3 bits (103), Expect = 0.008
Identities = 93/485 (19%), Positives = 172/485 (35%), Gaps = 80/485 (16%)

```

Query: 234 GQTISLDEFRLNSLWEPRWDSNVGKLKTTNADIRFNTKSES-----LLVKEDYAGGAR 287
      G T +++ R+E+ W      S V L      + + T +E+      L VK      +G
Sbjct: 536 GITKTVNALRIEDGTWTVTGSSAVNSLHLQAGKVAYATPAETNGKFKHLRVKT-LSGSG 594

Query: 288 FRFAYDPKEAKNTALIFEKNVTGTSDIIFENP-----IDDLKSLD-----GHQIIKV 334
      F      +      L+      +G      ++      ++ L ++      G +
Sbjct: 595 FEMNASADLSDGDLVVSDEASGQHKVLVRGAGTEPTGVESLTLVELPKGSQAGFTLANR 654

Query: 335 NGTADKHAFRLSGKHQKGIYTLSQLQORPEGFLPKCKN-----AMIWRFMHNRLKPPIP 387
      G D AFR      G++ L      +      N      + IW      N L      +
Sbjct: 655 GGVVDAGAFRYRLTPDNGVWGLERTSQLSAVANAALNTGGVGAASSIYAKGNALSKRLG 714

```

Query: 388 YCALRLNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKG VQ--LGGEVFT 445
 LRL+ + RT +K + +D + + K V G+ G + G+
 Sbjct: 715 --ELRLDPGAGGFWGRTFAQK----QQLDNKAGRRFDQK---VYGFELGADHAIAGQQGR 765

Query: 446 WQNESNQLSIGLMGGQAEQRSTFHNPDNDLTGNNVKGFGAGVYATWHQLQDKQTGAYAD 505
 W +G + G R +F + + + ++ + A V G Y D
 Sbjct: 766 WH-----VGGLLYTRARRSFVDDGAGHTDSAIGAYAAYV-----ADNGFYFD 809

Query: 506 SWMQYQRFRR--RINTEDGTE---RFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQP 560
 S ++ RF + + D ++ + G+ A++EAG L + + +++P
 Sbjct: 810 STLRSARFENDFTVTATDAVSIRGKYRANGVGATLEAGKRFTLHDGW-----FVEP 860

Query: 561 QAQLTYLGVNG-KFSDSENAHVNLGSRQLQTRVGVOAKAQFSLYKNIAIEPFAAVNALY 619
 Q++++ +G + + N V G R+G+ + L K+ I+P+A ++ L
 Sbjct: 861 QSEVSLFHASGGTYRAANNLSVKDEGGTSAVLRGLGLATGRRIDLGKDRVIQPYATLSWLQ 920

Query: 620 HNKPFGEVMDGERRVINNKTAIESQLGVAVKIKSHLTLQATFNRTG---KHHQAKQ GAL 676
 E G V N + + LG + + L L A R + AK L
 Sbjct: 921 -----EFKGVTTVRTNGYGLRTDLG--GGRAELALGLAAALGRGHSLYTSY EYAKGSKL 972

Query: 677 NLQWT 681
 L WT
 Sbjct: 973 TLPWT 977

tr Q9JMS5 YcbB protein [ycbB] [Escherichia coli] 1758 AA
align

Score = 43.5 bits (101), Expect = 0.013

Identities = 29/112 (25%), Positives = 54/112 (47%), Gaps = 12/112 (10%)

Query: 437 VQLGGEVFTWQNESNQLSIGLMG--QAEQRSTFHNPDNDLTGNNVKGFGAGVYATWHQ 494
 + +GG+++ W + N IG+MG G A ++T N + TGNV G+ G+Y + Q
 Sbjct: 1499 MMIGGDIYNWTDGYNYSHIGIMGGMGAANKTTSTN---NKRATGNVDGYTLGLYHV FQQ 1555

Query: 495 -----LQDKQTGAYADSWMQYQRFRRHRI-NTEDGTERFTSKGITASIEAGY 539
 + ++ G + S +QY + + + +T + + G + E GY
 Sbjct: 1556 NISDGLNESERQGLWYSSIQYMDYDNSVSSTNNFKANYGVNGFRLTGEVGY 1607

tr Q9XD84 TibA [tiba] [Escherichia coli] 989 AA
align

Score = 43.1 bits (100), Expect = 0.017

Identities = 50/210 (23%), Positives = 86/210 (40%), Gaps = 26/210 (12%)

Query: 393 LNNKNSDIFDRTLPRKGLWLRVIDGHSNQWVQGKTAPVEGYRKG VQLGGEVFTWQNESNQ 452
 L ++ D+ T G+W R G N+ G ++ + G + G ++ ++S+
 Sbjct: 711 LRFRHGDVMQNTAPGGVWGRYT-GSDNRISGGASSGYTLTQNGFETGADMVFDLSDSS- 768

Query: 453 LSIGLMGGQAEQRSTFHNPDNDLTGNNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQR 512
 L++G ++ S H + NV G G+YATW G Y D ++Y R
 Sbjct: 769 LAVGTFFSYSDN-SIKHARGGKS---NVDSSGGGLYATWFD---NDGYYVDGVLKYNR 819

Query: 513 FRHRINT--EDGTE---RFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYL 567

F + + T DGT ++ G S+EAG L E+ + QP + T
 Sbjct: 820 FNNELRTWMSDGTAVKGDYSQNGFGGSLEAGRTFSLNEN-----AWAQPYVRTTAF 870
 Query: 568 GVNGKFSSENNAHVNLLG-SRQLQTRVG VQ 596
 + K N +G ++ LQ G++
 Sbjct: 871 RADKKEIRLNNGMKASIGATKSLQAEAGLK 900

tr Q6G428 **Hypothetical protein [BH05510] [Bartonella henselae** 874
(Rochalimaea AA
henselae)] align

Score = 42.4 bits (98), Expect = 0.029

Identities = 54/225 (24%), Positives = 90/225 (40%), Gaps = 42/225 (18%)

Query: 479 GNVKG---FGAGVYATWHQLQDKQTGAYADSWMQYQRFRRHINTEDGTE-----RFTSKG 530
 G V G + G YAT+ ++G Y DS ++Y ++++ + + G
 Sbjct: 671 GGVSGINTYSIGAYATYFD---KSGWYLDLSILKYNQYQNNLKAVSTNGIAIEGNYNQWG 726

Query: 531 ITASIEAGYNALLAEHFTKKGNSLRVYLQPPAQLTYLGVNG---KFSDSENNAHVNLLGSR 587
 + S EAGY TK ++QP AQL++L V G K S+ +N S
 Sbjct: 727 LGTSFEAGYRF----ETTKSS-----WMQPYAQLSWLQVEGKEIKLSNEMTGDINAFTS- 776

Query: 588 QLQTRVG VQAKAQFSLYKNIAIEPFAAVNALYHNKPFVEMDGERRVINNKTAIESQL-- 645
 L++ VG+ A +F L ++ + L N+ D IN + L
 Sbjct: 777 -LRSEVGLSAGYEFCLGGDVTSMA YITAAWLREN-----DSNHTTINKLHQFVTDLSG 829

Query: 646 -----GVAVKIKSHLTLQATFNRQTG-KHHQAKQGALNLQWTF 682
 G++ + L A G K Q+ QG L ++++F
 Sbjct: 830 NFGKLGIGLSSLVSKKFKLYABEAQYVKGDKVKQSFQGILGVRYSF 874

tr Q83JR2 **Exported serine protease SigA [sigA] [Shigella** 1285 AA
flexneri] align

Score = 42.4 bits (98), Expect = 0.029

Identities = 71/307 (23%), Positives = 124/307 (40%), Gaps = 48/307 (15%)

Query: 393 LNNKNSDIFDRTLPRKGLWLRVIDGH---SNQWVQGKTAPVEGYRKG VQLGG-EVFTWQN 448
 LN + D+ D T G W R++ G S + T G K +L G ++FT
 Sbjct: 1010 LNKRMGDLRD-TNGEAGAWARIMSGAGSASGGYSDNYTHVQIGVDKKHELDGLDLFT--- 1065

Query: 449 ESNQLSIGLMGGQAEQRSTFHNPD TDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWM 508
 GL + ++ N +G K GAG+YA+ +GAY D
 Sbjct: 1066 -----GLTMTYTD SHAS-----SNAFSGKTKSVGAGLYAS-----AIFDSGAYIDLIS 1108

Query: 509 QYQRFRRHINTED---GTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPPAQLT 565
 +Y + + GT+ ++S + EAGY H T+ +++PQA+L
 Sbjct: 1109 KYVHHDNEYSATFAGLGTKDYSSHSLYVGA EAGYRY---HVTEDS-----WIEPQAE LV 1159

Query: 566 YLGVNGKFSSENNAHVNLL----GSRQLQTRVG VQAKAQFSLYKNIAIEPFAAVNALY-- 619
 Y V+GK D ++ +++ L R GV FS K+ + A + +
 Sbjct: 1160 YGAVSGKRFDWQDRGMSVTMKDKDFNPLIGRTGVDVGKSFS-GKDWKVTARAGLG YQFDL 1218

Query: 620 --HNKPFVEMDGERRVINNKTA-IESQLGVAVKIKSHLTLQATFNRQT-GKHHQAKQGA 675

++ + GE+R+ K I +G+ +I+ +L F + GK++
Sbjct: 1219 FANGETVLRDASGEKRIKGEKDGRILMNVLNAEIRDNLRFGLFEKSAFGKYNVDNAIN 1278
Query: 676 LNLQWTF 682
N +++F
Sbjct: 1279 ANFRYSF 1285

tr Q9L8L1 Exported serine protease SigA [sigA] [Shigella flexneri 2a] 1285 AA

align

Score = 42.4 bits (98), Expect = 0.029

Identities = 71/307 (23%), Positives = 124/307 (40%), Gaps = 48/307 (15%)

Query: 393 LNNKNSDIFDRTLPRKGLWLRVIDGH---SNQWVQKTAPVEGYRKGVLGG-EVFTWQN 448
LN + D+ D T G W R++ G S + T G K +L G ++FT
Sbjct: 1010 LNKRMGDLRD-TNGEAGAWARIMSGAGSASGGYSDNYTHVQIGVDKKHELDGLDLFT--- 1065
Query: 449 ESNQLSIGLMGGQAEQRSTFHNPDNDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWM 508
GL + ++ N +G K GAG+YA+ +GAY D
Sbjct: 1066 -----GLTMTYTDSHAS-----SNAFSGKTKSVGAGLYAS----AIFDSGAYIDLIS 1108
Query: 509 QYQRFRRHINTED---GTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLT 565
+Y + + GT+ ++S + EAGY H T+ +++PQA+L
Sbjct: 1109 KYVHHDNEYSATFAGLGTKDYSSHSYVGAEGYRY----HVTEDS-----WIEPQAEELV 1159
Query: 566 YLGVNGKFSDSENAHVNLL---GSRQLQTRVGVQAKAQFSLYKNIAIEPFPAVNALY-- 619
Y V+GK D ++ +++ L R GV FS K+ + A + +
Sbjct: 1160 YGAVSGKRFDWQDRGMSVTMKDKDFNPLIGRTGVDVGKSFS-GKDWKVTARAGLGYQFDL 1218
Query: 620 --HNKPFGEVMDGERRVINNKTA-IESQLGVAVKIKSHLTLQATFNRT-GKHHQAKQGA 675
+ + + GE+R+ K I +G+ +I+ +L F + GK++
Sbjct: 1219 FANGETVLRDASGEKRIKGEKDGRILMNVLNAEIRDNLRFGLFEKSAFGKYNVDNAIN 1278
Query: 676 LNLQWTF 682
N +++F
Sbjct: 1279 ANFRYSF 1285

tr Q7C013 Serine protease [sigA] [Shigella flexneri] 1285 AA
align

Score = 42.4 bits (98), Expect = 0.029

Identities = 71/307 (23%), Positives = 124/307 (40%), Gaps = 48/307 (15%)

Query: 393 LNNKNSDIFDRTLPRKGLWLRVIDGH---SNQWVQKTAPVEGYRKGVLGG-EVFTWQN 448
LN + D+ D T G W R++ G S + T G K +L G ++FT
Sbjct: 1010 LNKRMGDLRD-TNGEAGAWARIMSGAGSASGGYSDNYTHVQIGVDKKHELDGLDLFT--- 1065
Query: 449 ESNQLSIGLMGGQAEQRSTFHNPDNDNLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWM 508
GL + ++ N +G K GAG+YA+ +GAY D
Sbjct: 1066 -----GLTMTYTDSHAS-----SNAFSGKTKSVGAGLYAS----AIFDSGAYIDLIS 1108
Query: 509 QYQRFRRHINTED---GTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLT 565

```

      +Y      +      +      GT+ ++S      +      EAGY      H T+      +++PQA+L
Sbjct: 1109 KYVHHDDNEYSATFAGLGTKDYSSHSYVGAEEAGYRY----HVTEDS-----WIEPQAELV 1159

Query: 566 YLGVNGKFSSENHVNLL----GSRQLQTRVGQVQAKAQFSLYKNIAIEPFAAVNALY-- 619
      Y V+GK D ++ +++      L R GV      FS K+ + A + +
Sbjct: 1160 YGAVSGKRFDWQDRGMSVTMKDKDFNPLIGRTGVDVGKSFS-GKDWKVTARAGLGYQFDL 1218

Query: 620 --HNKPFGVEMDGERRVINNKTA-IESQLGVAVKIKSHLTLQATFNRQT-GKHHQAKQGA 675
      + +      + GE+R+ K I' +G+ +I+ +L      F + GK++
Sbjct: 1219 FANGETVLRDASGEKRIKGEKDGRILMNVLNAEIRDNLRFGLFEKSAFGKYNVDNAIN 1278

Query: 676 LNLQWTF 682
      N +++F
Sbjct: 1279 ANFRYSF 1285

```

```

tr Q8UJW1 Autotransporter protein [yapE] [Agrobacterium tumefaciens      868
      (strain AA
      C58 / ATCC 33970)] align

```

Score = 40.0 bits (92), Expect = 0.14

Identities = 66/293 (22%), Positives = 113/293 (38%), Gaps = 46/293 (15%)

```

Query: 411 WLRVIDGHSNQWVQGKTAP-VEGYRKGVLGGEVFTWQNESNQLS-IGLMGGQAEQRSTF 468
      W R      ++      G +P +G G+Q G ++ + E+      GL G +
Sbjct: 599 WARTFGQNTWKWDGTVSPSFDGNLFGLQAGQDLLGRETEAGGFDRFGLFVGYSRMNGDI 658

Query: 469 HNPDT--DNLTGTVKGFAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTEDGTE-R 525
      +NL G V G A W + + G Y D+ + F + G
Sbjct: 659 KGQALGWNVLAVGEVDIGGTSFGAYWTHVGAQ--GWYLDVLMGTWFSGDATSRAGESVN 716

Query: 526 FTSGKITASIEAGYNALLAEHFTKKGNSLRVYLQPPAQLTYLGVN-----GKFS-----DS 576
      + AS+E GY L E +T      L+PQAQ+ + ++      +FS DS
Sbjct: 717 IDGSSVAASLEGGYPIALTEDWT-----LEPQAQIIWQKLSLDDEADRFSSVAFDS 767

Query: 577 ENAHVNLLGSR---QLQTRVG-VQAKAQFSLYKNIAIEPFAAVNALYHNKPFGVEMDGER 632
      +NA LG R QT G +Q + +++ + + + N P E G
Sbjct: 768 DNAVTGRLGVRLQGNQYQTDGSLIQPYLKANIIWHGFSSDQMTR----FDNDPIVTETGG-- 821

Query: 633 RVINNKTATIESQLGVAVKIKSHLTLQATFNRQT---GKHHQAKQG--ALNLQW 680
      T++E G+ + +++ AT + T G+ +A +G LN++W
Sbjct: 822 -----TSLEIGGGLVASLTEKVSVFATVDYTTNLGGERKRAIEGNIGLNIKW 868

```

```

tr Q7D396 AGR_pAT_528p [AGR_pAT_528] [Agrobacterium tumefaciens (strain      921
      C58 / AA
      ATCC 33970)] align

```

Score = 40.0 bits (92), Expect = 0.14

Identities = 66/293 (22%), Positives = 113/293 (38%), Gaps = 46/293 (15%)

```

Query: 411 WLRVIDGHSNQWVQGKTAP-VEGYRKGVLGGEVFTWQNESNQLS-IGLMGGQAEQRSTF 468
      W R      ++      G +P +G G+Q G ++ + E+      GL G +
Sbjct: 652 WARTFGQNTWKWDGTVSPSFDGNLFGLQAGQDLLGRETEAGGFDRFGLFVGYSRMNGDI 711

```

Query: 469 HNPDT--DNLTGTVKGFAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTEDGTE-R 525
 +NL G V G A W + + G Y D + + F + G
 Sbjct: 712 KGQALGWNNAVGEVDIGGTSFGAYWTHVGAQ--GWYLDVAVLMGTWFGSDATSRAGESVN 769

Query: 526 FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPAQLTYLGVN-----GKFS----DS 576
 + AS+E GY L E +T L+PQAQ+ + ++ +FS DS
 Sbjct: 770 IDGSSVAASLEGGYPIALTEDWT-----LEPQAQIIWQKLSLDDEADRFSSVAFDS 820

Query: 577 ENAHVNLLGSR---QLQTRVG-VQAKAQFSLYKNIAIEPFAAVNALYHNKPFGEVMDGER 632
 +NA LG R QT G +Q + +++ + + + N P E G
 Sbjct: 821 DNAVTGRLGVRLQGNVYQTDGLIQPYLKANIWHGFSSDQMTR----FDNDPIVTETGG-- 874

Query: 633 RVINNKTAIESQLGVAVKIKSHLTLQATFNRT---GKHHQAKQG--ALNLQW 680
 T++E G+ + +++ AT + T G+ +A +G LN++W
 Sbjct: 875 -----TSLEIGGGLVASLTEKVSFATVDYTTNLGGERKRAIEGNIGLNLIKW 921

tr Q7WK90 Autotransporter [phg] [*Bordetella bronchiseptica* (*Alcaligenes bronchisepticus*)]

align

Score = 39.7 bits (91), Expect = 0.19

Identities = 43/213 (20%), Positives = 85/213 (39%), Gaps = 49/213 (23%)

Query: 446 WQNESNQLSIGLMGGQAEQRSTFHNPDNDNLTGTVKGFAGVYATWHQLQDKQTGAYAD 505
 W+ ++ +L +G G + R D +++ G ++ G Y T+ G Y D
 Sbjct: 204 WRLDTGRLLYGAYAGVSRARM-----DDNDIMHGRIESRFLGTYLTYVD----NGGFYVD 254

Query: 506 SWMQYQFRHRINTE-----DGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQ 559
 + + R ++ + D + + T S+EAGY+ L + R +++
 Sbjct: 255 AVSKLGRIDESVSFDLPLGLGDYDDDISHTTYTGVSVEAGYHFKLPQ-----RWFVE 305

Query: 560 PQAQLTYLGVNGKFSSENHAVNLLGSRQLQTRVGVAQAKAQFSLYKNIAIEPFAAVNALY 619
 PQAQ+ Y S ++ ++ G R GV+A F+L + P+ + + L+
 Sbjct: 306 PQAQVIY-----SRSSQTSVQG-----RAGVRAGRDFTLGGATLRPYVSASYLH 350

Query: 620 H-----NKPFGVEMDGERRVINNKTAIE 642
 K + E+ G R + A++
 Sbjct: 351 EFSHDDSVDFGGKSYDAELPGSRWQLGAGAALD 383

tr Q7W8X9 Autotransporter [phg] [*Bordetella parapertussis*] 415 AA
align

Score = 39.7 bits (91), Expect = 0.19

Identities = 43/213 (20%), Positives = 85/213 (39%), Gaps = 49/213 (23%)

Query: 446 WQNESNQLSIGLMGGQAEQRSTFHNPDNDNLTGTVKGFAGVYATWHQLQDKQTGAYAD 505
 W+ ++ +L +G G + R D +++ G ++ G Y T+ G Y D
 Sbjct: 204 WRLDTGRLLYGAYAGVSRARM-----DDNDIMHGRIESRFLGTYLTYVD----NGGFYVD 254

Query: 506 SWMQYQFRHRINTE-----DGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQ 559
 + + R ++ + D + + T S+EAGY+ L + R +++
 Sbjct: 255 AVSKLGRIDESVSFDLPLELGDYDDDISHTTYTGVSVEAGYHFRLPQ-----RWFVE 305

Query: 560 PQAQLTYLGVNGKFSSENHVNLLGSRQLQTRVGVQAKAQFSLYKNIAIEPFAAVNALY 619
 PQAQ+ Y S ++ ++ G R GV+A F+L + P+ + + L+
 Sbjct: 306 PQAQVIY-----SRSSQTSVQG-----RAGVRAGRDFTLGGATLRPYVSASYLH 350

Query: 620 H-----NKPFGEVMDGERRVINNKTAIE 642
 K + E+ G R + A++
 Sbjct: 351 EFSHDDSVDFGGKSYDAELPGSRWQLGAGAALD 383

tr Q84GK0 **Secreted autotransporter protein EatA [eatA] [Escherichia coli]** 1364
 AA
align

Score = 39.7 bits (91), Expect = 0.19

Identities = 77/350 (22%), Positives = 136/350 (38%), Gaps = 53/350 (15%)

Query: 244 LENSLEPRWDSNVGKLKTTNADIRFNTKSE--SLLVKEDYAGGARFRFAYDPKEAKNTA 301
 + N+LW +S + +LK ++ I + L VKE A + F + +A
 Sbjct: 928 MNNALWHSRNSSELKELKANDSQIELGVRGHFAKLRVKELIASNSVFLVHANNSQADQ-- 985

Query: 302 LIFEKNVTGTSDIIFENPIDDLKSLDGHQIIVNGTADKHAFRLSGKHQKGIYTLSQLQR 361
 L + G+++ I + + + +I +D++ F+ +G Q G ++ + R
 Sbjct: 986 LNVTDKLGQSNNTILVDFFNKAANGTNVTLLITAPKGSIDENTFK-AGTQQIGFSNITPEIR 1044

Query: 362 PEGF-----LPKCKNAMIWRFMHNRLKPPIPYCALRLNNKNSDIFDRTLPRKGLW 411
 E +A + + + +NN N + D
 Sbjct: 1045 TENTDTATQWVLTGYQSVADARASKIATDFMDSGYKSFLTEVNNLNKRMGD----- 1095

Query: 412 LRVIDGHSNQWVQ---GKTAPVEGYRKG---VQLGGEVFTWQNESNQLSIGLMGGQAEQR 465
 LR G + W + G + GYR VQ+G + ++E N I L G
 Sbjct: 1096 LRDSQGDAGGARIMNGTSGESGYRDNYTHVQIGADR---KHELN--GIDLFTGALLTY 1150

Query: 466 STFHNPDNDLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRF--RHRINTEDGT 523
 + N + +G K G GVYA+ ++GAY D +Y R+ +N
 Sbjct: 1151 TD--NNASSQAFSGKTKSLGGGVYASGLF----ESGAYFDLIGKYLHHDNRYTLNFASLG 1204

Query: 524 ER-FTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGK 572
 ER +TS + A E GY ++E+ +++PQ +L Y V+GK
 Sbjct: 1205 ERSYTSLSLYAGAEIGYRYHMSSEN-----TWVEPQMELVYGSVSGK 1245

tr Q8UJX1 **Autotransporter protein [bapA] [Agrobacterium tumefaciens (strain C58 / ATCC 33970)]** 1035
 AA
align

Score = 39.3 bits (90), Expect = 0.25

Identities = 49/199 (24%), Positives = 83/199 (41%), Gaps = 32/199 (16%)

Query: 409 GLWLRVIDGHSNQWVQGKTAPVEGYRKGV---QLGGEVFTWQNESNQL---SIGLMGGQ 461
 G+W R+ H++ + A E Y + V Q G + + ES +L ++ G+
 Sbjct: 759 GVGRIEGVHNHIEPRFSAAAAE-YDQNVFKLQAGIDGLLTETESGKLIGGFTVHYAHGK 817

Query: 462 AEQRSTFHNPDTNDLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFRRHRINTED 521
 + RS + + + + G+G G TW+ + G Y D Q + +N+
 Sbjct: 818 TDTRSVWGDGEI-----STDGYLGGTTLTWYG----ENGFYLDGQAQMTWYTSGLNSLL 867

Query: 522 GTERFTSK---GITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVN-GKFSDS 576
T G T S+E+G + ++ + PQAQL Y V+ F+D+
Sbjct: 868 ARTNLTDNNDGFGYTLSLESGTRIAIDPGWS-----VTPQAQLVYSNVDFDAFTDT 918

Query: 577 ENAHVNLLGSRQLQTRVGV 595
A V+L LQ R+GV
Sbjct: 919 FGARVSLDRGESLQGR LGV 937

tr Q7D3A2 AGR_pAT_511p [AGR_pAT_511] [Agrobacterium tumefaciens (strain 1192
C58 / AA
ATCC 33970)] align

Score = 39.3 bits (90), Expect = 0.25
Identities = 49/199 (24%), Positives = 83/199 (41%), Gaps = 32/199 (16%)

Query: 409 GLWLRVIDGHSNQWVGKTAPVEGYRKGV---QLGGEVFTWQNESNQL---SIGLMGGQ 461
G+W R+ H++ + A E Y + V Q G + + ES +L ++ G+
Sbjct: 916 GVGRIEGVHNHIEPRFSAAAAE-YDQNVFKLQAGIDGLLTETESGKLIGGFTVHYAHGK 974

Query: 462 AEQRSTFHNPDTDNLTGNGVKGFGAGVYATWHQLQDKQTGAYADSWMQYQRFHRINTED 521
+ RS + + + + G+G G TW+ + G Y D Q + +N+
Sbjct: 975 TDTRSVWGDGEI-----STDGYGLGGTLTWYG----ENGFYLDGQAQMTWYTSGLNSLL 1024

Query: 522 GTERFTSK---GITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVN-GKFSDS 576
T G T S+E+G + ++ + PQAQL Y V+ F+D+
Sbjct: 1025 ARTNLTDNNDGFGYTLSLESGTRIAIDPGWS-----VTPQAQLVYSNVDFDAFTDT 1075

Query: 577 ENAHVNLLGSRQLQTRVGV 595
A V+L LQ R+GV
Sbjct: 1076 FGARVSLDRGESLQGR LGV 1094

tr Q6MTD5 Hypothetical transmembrane protein [MSC_0473] [Mycoplasma 873
mycoides AA
(subsp. mycoides SC)] align

Score = 38.9 bits (89), Expect = 0.32
Identities = 45/181 (24%), Positives = 74/181 (40%), Gaps = 24/181 (13%)

Query: 27 FFSILYTSPLLAVDYVYDKTKLTNDEITRLKKLRDKTSEYWKKEITYLITEDNPKVPPFPA 86
F ++ + L ++ + KTKLT ++ +LKK +DK Y K+ +IT K
Sbjct: 182 FNDLMLSFYLSRIENLNTKTKLTAKDLAKLKKFKDKYDFYLNKQEIIITNKKLK-----Q 236

Query: 87 LYPRTYQFENINNSKKISFYDQEYTEGYLVGFARGLGVAKRNGDTEEQIRKYFKECFNSN 146
L Y E +N K++ + +Y E YL + +EQI K
Sbjct: 237 LKKDQYNLELVN--KRLLKLENKY-EIYL-----NKQEIQINNNKKAKLLKK 279

Query: 147 TKIRDY-STCQAEKFGSHPLIVKSHIFSLGPKIKNSHINSEILSVGNYTEWANQVIHHIE 205
K + + C + I+ + F+ IKNS I E L ++QV+ +E
Sbjct: 280 KKSEBIKNKCLLKLENKKQKIINKNSFTKS-SIKNSLIKQEFLQARINKNTSSQVLETLE 338

Query: 206 N 206
N

Sbjct: 339 N 339

sp P45386 Immunoglobulin A1 protease precursor (EC 3.4.21.72) (IGA1 1849
IGA4_HAEIN protease) AA
[iga] [Haemophilus influenzae] align

Score = 38.5 bits (88), Expect = 0.42

Identities = 34/142 (23%), Positives = 59/142 (40%), Gaps = 20/142 (14%)

Query: 235 QTISLDEFRL-ENSLWEPRWDSNVGKLKTTNADIRFNTKSE-----SLLVKEDYAGGA 286
Q+I + L ENS W +SNV +L TN I N +++ + L +G

Sbjct: 852 QSIGTSQVNLKENSHWHLTGNSNVNQLNLTNGHIHLNAQNDANKVTTYNTLTVNSLSGNG 911

Query: 287 RFRFAYDPKEAKNTALIFEKNVTG-----TSDIIFENPIDDLKSLDGH-----QIIKV 334
F + D K+ ++ K+ TG +D E ++L D ++

Sbjct: 912 SFYYWVDFTNNKSNKVVVNKSATGNFTLQVADKTGEPNHNELTLFDASNATRNNEVTLA 971

Query: 335 NGTADKHAFRLSGKHQKGIYTL 356

NG+ D+ A++ ++ G Y L

Sbjct: 972 NGSVDRGAWKYKLNRVNGRYDL 993

tr Q9Z5R3 Phg protein (Autotransporter) [phg] [Bordetella pertussis] 418 AA

align

Score = 38.1 bits (87), Expect = 0.55

Identities = 43/213 (20%), Positives = 84/213 (39%), Gaps = 49/213 (23%)

Query: 446 WQNESNQLSIGLMGGQAEQRSTFHNPDNDLTTGNVKGFGAGVYATWHQLQDKQTGAYAD 505
W+ ++ +L +G G + R D +++ G ++ G Y T+ G Y D

Sbjct: 207 WRLDTGRLLYGAYAGVSRARM-----DDNDIMHGRIESRFLGTYLTYVD----NGGFYVD 257

Query: 506 SWMQYQRFRRHRINTE-----DGTERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQ 559
+ + R ++ + D + + T S EAGY+ L + R +++

Sbjct: 258 AVSKLGRIDESVSFDLPLGLGDYDDDISHTTYTGSAEAGYHFKLPQ-----RWFVE 308

Query: 560 PQAQLTYLGVNGKFSSENHVNLLGSRQLQTRVGVAQAQFSLYKNIAIEPFAAVNALY 619
PQAQ+ Y S ++ ++ G R GV+A F+L + P+ ++ L+

Sbjct: 309 PQAQVIY-----SRSSQTSVQG-----RAGVRAGRDFTLGGATLRPYVSASYLH 353

Query: 620 H-----NKPFGVEMDGERRVINNKTAIE 642

K + E+ G R + A++

Sbjct: 354 EFSHDDSVDFGGKSYDAELPGSRWQLGAGAALD 386

tr Q6KD18 Antigen 43 precursor Sap [sap] [Escherichia coli] 1042 AA

align

Score = 37.7 bits (86), Expect = 0.71

Identities = 38/156 (24%), Positives = 65/156 (41%), Gaps = 14/156 (8%)

Query: 417 GHSNQW--VQKGTAPVEGYRKGVLGGVFTWQNESNQLSIGLMGGQAEQRSTFHNPD TD 474
 GH N V+G T G V+L G++ + L+ G+ G A S+ D D
 Sbjct: 757 GHDNNGGIVRGATPESSGSYGFVRLEGDLLRTEVAGMSLT TG VYG--AAGHSSVDVKDDD 814

Query: 475 NLTTGNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTEDGTERFTSKGITAS 534
 G V+ AG + L +G +AD Q R + ++++ R +G S
 Sbjct: 815 GSRAGTVRD-DAGSLGGYLN LVHTSSGLWADIVAQGRHSMKASSDNNDFRARGRGWQGS 873

Query: 535 IEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVN 570
 +E G + ++ + L+PQ Q T+ G++
 Sbjct: 874 LETGLPFSITDN-----LMLEPQLQYTWQGLS 900

tr Q8FDW4 Acreted auto transpoter toxin [sat] [Escherichia coli O6] 1299 AA

align

Score = 37.0 bits (84), Expect = 1.2
 Identities = 66/290 (22%), Positives = 114/290 (38%), Gaps = 40/290 (13%)

Query: 412 LRVIDGHSNQW---VQKGTAPVEGYRKG---VQLGGVFTWQNESNQLSIGLMGGQAEQR 465
 LR I+G S W + G + G+ VQ+G + N+ + L G
 Sbjct: 1031 LRDINGESGAWARIISGTGSAGGGFSDNYTHVQVGAD-----NKHELDGLDLFTGVTMTY 1085

Query: 466 STPHNPDTDNLTGNNVKGFGAGVYATWHQLQDKQTGAYADSWMQYQFRHRINTED---G 522
 + H + +G K GAG+YA+ ++GAY D +Y + G
 Sbjct: 1086 TDSHAGS--DAFSGETKSVGAGLYAS----AMFESGAYIDLIGKYVHHDNEYTATFAGLG 1139

Query: 523 TERFTSKGITASIEAGYNALLAEHFTKKGNSLRVYLQPQAQLTYLGVNGKFSDSENAHVN 582
 T ++S A E GY H T +++PQA+L Y V+GK ++ +N
 Sbjct: 1140 TRDYSSHSWYAGAEVGYRY----HVTDSA-----WIEPQAEVYGA VSGKQFSWKDQGMN 1190

Query: 583 LL----GSRQLQTRVG VQAKAQFSLYKNIAIEPFAAVNALY-----HNKPFGVEMDGERRV 634
 L L R GV FS K+ + A + + + + + GE+R+
 Sbjct: 1191 LTMKDKDFNPLIGRTGVDVGKSFS-GKDWKVTARAGLGYQFDLFANGETVLRDASGEKRI 1249

Query: 635 INNKTA-IESQLGVAVKIKSHLT LQATFNRT-GKHHQAKQGALNLQWTF 682
 K + +G+ +I+ +L F + GK++ N +++F
 Sbjct: 1250 KGEKDGRMLMNVGLNAEIRDNLRFGLFEKSAFGKYNVDNAINANFRYSF 1299

Database: EXPASY/UniProt

Posted date: Sep 12, 2004 1:43 PM

Number of letters in database: 501,960,298

Number of sequences in database: 1,568,464

Lambda K H
 0.317 0.135 0.401

Gapped

Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

length of query: 682
length of database: 501,960,298
effective HSP length: 131
effective length of query: 551
effective length of database: 296,491,514
effective search space: 163366824214
effective search space used: 163366824214
T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 77 (34.3 bits)

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Entry information

Entry name **INVA_YEREN**
 Primary accession number **P19196**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 16, November 1990
 Sequence was last modified in Release 16, November 1990
 Annotations were last modified in Release 40, October 2001

Name and origin of the protein

Protein name **Invasin**
 Synonyms None
 Gene name None
 From Yersinia enterocolitica [TaxID: 630]
 Taxonomy Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=8081C / Serotype O:8;
MEDLINE=91041720;PubMed=2233250 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Young V.B., Miller V.L., Falkow S., Schoolnik G.K.;
 "Sequence, localization and function of the invasin protein of Yersinia enterocolitica.";
 Mol. Microbiol. 4:1119-1128(1990).

Comments

- **FUNCTION:** Invasin is a protein that allows enteric bacteria to penetrate cultured mammalian cells. The entry of invasin in the cell is mediated by binding several beta-1 chain integrins.
- **SUBCELLULAR LOCATION:** Outer membrane.
- **SIMILARITY:** Belongs to the intimin/invasin family.

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Cross-references

EMBL X53368; CAA37448.1; -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
 PIR S11442; S11442.
 HSSP P11922; 1CWV. [[HSSP ENTRY](#) / [PDB](#)]
 IPR003344; Big_1.
 InterPro IPR003535; Intimin.
 IPR008964; Invasin_intimin.
[Graphical view of domain structure.](#)
 Pfam PF02369; Big_1; 1.
[Pfam graphical view of domain structure.](#)
 PRINTS PR01369; INTIMIN.
 SMART SM00634; BID_1; 1.
 ProDom [[Domain structure](#) / [List of seq. sharing at least 1 domain](#)]
 HOBACGEN [[Family](#) / [Alignment](#) / [Tree](#)]
 BLOCKS P19196.
 ProtoNet P19196.
 ProtoMap P19196.
 PRESAGE P19196.
 DIP P19196.
 ModBase P19196.
 SMR P19196; 6133FF9FDB8D9BBA.
 SWISS-2DPAGE [Get region on 2D PAGE.](#)
 UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Outer membrane.

Features

None

Sequence information

Length: 835 Molecular weight: 91361 CRC64: 6133FF9FDB8D9BBA [This is a checksum on the
 AA Da sequence]

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70	80	90	100	110	120
TSLAVSGNAS	NITRSMVND A	ANQEVKHWLN	RFGTTQVNVN	FDKKFSLKES	SLDWLLPWYD
130	140	150	160	170	180
SASYVFFSQL	GIRNKDSRNT	LNIGAGVRTF	QQSWMYGFNT	SYDNDMTGHN	HRIGVGAEAW
190	200	210	220	230	240
TDYLQLSANG	YFRLNGWHQS	RDFADYNERP	ASGGDIHVKA	YLPALPQLGG	KLKYEQYRGE
250	260	270	280	290	300

```

RVALFGKDNL QSNPYAVTTG LIYTPIPFIT LGVDQRMGKS RQHEIQWNLQ MDYRLGESFR
      310      320      330      340      350      360
      |      |      |      |      |      |
SQFSPAUVAG TRLLAESRYN LVERNPNI VL EYQKQNTIKL AFSPA VLSGL PGQVYSVSAQ
      370      380      390      400      410      420
      |      |      |      |      |      |
IQSQSALQRI LWND AQWVAA GGKLIPVSAT DYNVVLPPYK PMAPASRTVG KTGESEAAVN
      430      440      450      460      470      480
      |      |      |      |      |      |
TYTLSATAID NHGNSSNPAT LTVIVQQPQF VITSEVTDDG ALADGRTPIT VKFTVTNIDS
      490      500      510      520      530      540
      |      |      |      |      |      |
TPVAEQEGVI TTSNGALPSK VTKKTDAGV ISIALTSFTV GVS VVTLDIQ GQQATVDVRF
      550      560      570      580      590      600
      |      |      |      |      |      |
AVLPPDVTNS SFNVSPSDIV ADGSMQSILT FVPRNKNEF VSGITDLEFI QSGVPVTISP
      610      620      630      640      650      660
      |      |      |      |      |      |
VTENADNYTA SVVGNSVG DV DITPQVGGES LDLLQKRITL YPVPKITGIN VNGEQFATDK
      670      680      690      700      710      720
      |      |      |      |      |      |
GFPKTTFNKA TFQLVMNDDV ANNTQYDWTS SYAASAPVDN QGKVNIA YKT YGSTVTVTAK
      730      740      750      760      770      780
      |      |      |      |      |      |
SKKFPSYTAT YQFKPNLWVF SGTMSLQSSV EASRNCQRTD FTALIESARA SNGSRSPDGT
      790      800      810      820      830
      |      |      |      |      |
LWGEWGSLAT YDSAEWPSGN YWTKKTSTDF VTMDMTTGDI PTSAATAYPL CAEPQ

```

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[Dotlet \(Java\)](#)



[ScanProsite](#), [MotifScan](#)



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[\[Keywords\]](#)
[\[Features\]](#)
[\[Sequence\]](#)
[\[Tools\]](#)

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Entry information

Entry name	INVA_YERPS
Primary accession number	P11922
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 12, October 1989
Sequence was last modified in	Release 12, October 1989
Annotations were last modified in	Release 45, October 2004
Name and origin of the protein	
Protein name	Invasin
Synonyms	None
Gene name	None
From	<u>Yersinia pseudotuberculosis</u> [TaxID: 633]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Gammaproteobacteria</u> ; <u>Enterobacteriales</u> ; <u>Enterobacteriaceae</u> ; <u>Yersinia</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
DOI=[10.1016/0092-8674\(87\)90335-7](#);MEDLINE=87301720;PubMed=3304658 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Isberg R.R.](#), [Voorhis D.L.](#), [Falkow S.](#);
"Identification of invasins: a protein that allows enteric bacteria to penetrate cultured mammalian cells.";
[Cell](#) 50:769-778(1987).
- [2] INTEGRIN-BINDING DOMAIN.
MEDLINE=90269235;PubMed=1693333 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Leong J.M.](#), [Fournier R.S.](#), [Isberg R.R.](#);
"Identification of the integrin binding domain of the Yersinia pseudotuberculosis invasins protein.";
[EMBO J.](#) 9:1979-1989(1990).
- [3] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 494-985.
DOI=[10.1126/science.286.5438.291](#);PubMed=10514372 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Hamburger Z.A.](#), [Brown M.S.](#), [Isberg R.R.](#), [Bjorkman P.J.](#);

"Crystal structure of invasin: a bacterial integrin-binding protein."; Science 286:291-295(1999).

Comments

- **FUNCTION:** Invasin is a protein that allows enteric bacteria to penetrate cultured mammalian cells. The entry of invasin in the cell is mediated by binding several beta-1 chain integrins.
- **SUBCELLULAR LOCATION:** Outer surface.
- **SIMILARITY:** Belongs to the intimin/invasin family.
- **CAUTION:** It is uncertain whether Met-1, Met-17 or Met-19 is the initiator.

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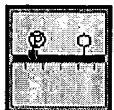
Cross-references

	M17448; AAA27633.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
EMBL	M17448; AAA27632.1; ALT_INIT. [EMBL / GenBank / DDBJ] [CoDingSequence]
	M17448; AAA27634.1; ALT_INIT. [EMBL / GenBank / DDBJ] [CoDingSequence]
	M17448; AAA27635.1; ALT_INIT. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	A29646; A29646.
PDB	1CWV; X-ray; A=494-985. [ExPASy / RCSB / EBI]
	IPR003344; Big_1.
InterPro	IPR003535; Intimin.
	IPR008964; Invasin_intimin.
	Graphical view of domain structure.
Pfam	PF02369; Big_1; 2.
	Pfam graphical view of domain structure.
PRINTS	PR01369; INTIMIN.
SMART	SM00634; BID_1; 2.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	P11922.
ProtoNet	P11922.
ProtoMap	P11922.
PRESAGE	P11922.
DIP	P11922.
ModBase	P11922.
SMR	P11922; C875941B24BD35EE.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

Keywords

3D-structure.

Features



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[Feature aligner](#)

Key	From	To	Length	Description
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DOMAIN	<u>494</u>	<u>985</u>	492	Extracellular.
DOMAIN	<u>494</u>	<u>594</u>	101	D1.
DOMAIN	<u>595</u>	<u>694</u>	100	D2.
DOMAIN	<u>695</u>	<u>794</u>	100	D3.
DOMAIN	<u>795</u>	<u>985</u>	191	Integrin-binding.
DOMAIN	<u>795</u>	<u>886</u>	92	D4.
DOMAIN	<u>887</u>	<u>985</u>	99	D5.
DISULFID	<u>906</u>	<u>981</u>		
STRAND	<u>503</u>	<u>509</u>	7	
STRAND	<u>513</u>	<u>514</u>	2	
STRAND	<u>521</u>	<u>528</u>	8	
TURN	<u>530</u>	<u>531</u>	2	
STRAND	<u>534</u>	<u>534</u>	1	
STRAND	<u>539</u>	<u>543</u>	5	
TURN	<u>546</u>	<u>547</u>	2	
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STRAND	<u>573</u>	<u>581</u>	9	
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Sequence information

Length: **985** Molecular weight: **106627** CRC64: **C875941B24BD35EE** [This is a checksum on the
AA **Da** sequence]

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70	80	90	100	110	120
QPYSVSSSAF	ENLHPNNEME	SSINPFSASD	TERNAAIIDR	ANKEQETEAV	NKMISTGARL
130	140	150	160	170	180
AASGRASDVA	HSMVGDAVNQ	EIKQWLNRFQ	TAQVNLNFDK	NFSLKESSLD	WLAPWYDSAS
190	200	210	220	230	240
FLFFSQLGIR	NKDSRNTLNL	GVGIRTLENG	WLYGLNTFYD	NDLTGHNHRI	GLGAEAWTDY
250	260	270	280	290	300
LQLAANGYFR	LNGWHSSRDF	SDYKERPATG	GDLRANAYLP	ALPQLGGKLM	YEQYTGERVA
310	320	330	340	350	360
LFGKDNLQRN	PYAVTAGINY	TPVPLLTGVV	DQRMGKSSKH	ETQWNLMQNY	RLGESFQSQL
370	380	390	400	410	420
SPSAVAGTRL	LAESRYNLVD	RNNNIVLEYQ	KQQVVKLTLS	PATISGLPGQ	VYQVNAQVQG
430	440	450	460	470	480
ASAVREIVWS	DAELIAAGGT	LTPLSTTQFN	LVLPPYKRTA	QVSRVTDDL	ANFYSLSALA
490	500	510	520	530	540
VDHQGNRSNS	FTLSVTVQQP	QLTLTAAVIG	DGAPANGKTA	ITVEFTVADF	EGKPLAQEV
550	560	570	580	590	600
VITTNNGALP	NKITEKTDAN	GVARIALTNT	TDGVTVVTAE	VEGQRQSVDT	HFVKGTIAAD
610	620	630	640	650	660
KSTLAAVPTS	IIADGLMAST	ITLELKDTYG	DPQAGANVAF	DTTLGNMGVI	TDHNDGTYS
670	680	690	700	710	720
PLTSTTLGVA	TVT VKVDGAA	FSVPSVTVNF	TADPIPDAGR	SSFTVSTPDI	LADGTMSSTL
730	740	750	760	770	780
SFVPVDKNGH	FISGMQGLSF	TQNGVPVSIS	PITEQPDSYT	ATVVGNSVGD	VTITPQVDTL
790	800	810	820	830	840
ILSTLQKKIS	LFPVPTLTGI	LVNGQNFATD	KGFPKTIFKN	ATFQLQMDND	VANNTQYEWS
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910	920	930	940	950	960
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970 980
| |
TMNMDTGALQ PGPAYLAFPL CALSI

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WEST Search History

DATE: Tuesday, September 14, 2004

Hide?	<u>Set</u> <u>Name</u>	<u>Query</u>	<u>Hit</u> <u>Count</u>
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L1	ipa\$1	29122
<input type="checkbox"/>	L2	L1 same (coli or shigella or salmonella or yersinia or rickettsia or brucella or erhlichiae or edwarsiella or campylobacter or legionella or neisseria)	479
<input type="checkbox"/>	L3	L2 and (invasin or intimin or yop)	71
<input type="checkbox"/>	L4	L3 and (lps or lipo-polysaccharide or lipopolysaccharide)	34
<input type="checkbox"/>	L5	('6245892' '20020197276' '6083683' '6680374' '6277379' '20010009957')!.PN.	10

END OF SEARCH HISTORY

Search Results - Record(s) 1 through 10 of 10 returned.

L5: Entry 1 of 10	File: PGPB	Dec 26, 2002
PGPUB-DOCUMENT-NUMBER: 20020197276 DOCUMENT-IDENTIFIER: US 20020197276 A1		
TITLE: Heterologous protection induced by immunization with invaplex vaccine PUBLICATION-DATE: December 26, 2002		
US-CL-CURRENT: <u>424/203.1</u> INT-CL: [07] <u>A61 K 39/116</u>		

L5: Entry 2 of 10	File: PGPB	Jul 26, 2001
PGPUB-DOCUMENT-NUMBER: 20010009957 DOCUMENT-IDENTIFIER: US 20010009957 A1		
TITLE: Invaplex from gram negative bacteria, method of purification and methods of use PUBLICATION-DATE: July 26, 2001		
US-CL-CURRENT: <u>530/395</u> ; <u>435/195</u> INT-CL: [07] <u>C12 N 9/14</u> , <u>C07 K 14/24</u>		

L5: Entry 3 of 10	File: USPT	Jan 20, 2004
US-PAT-NO: 6680374 DOCUMENT-IDENTIFIER: US 6680374 B2		
TITLE: Invaplex from gram negative bacteria, method of purification and methods of use		
DATE-ISSUED: January 20, 2004		
US-CL-CURRENT: <u>530/388.1</u> ; <u>424/130.1</u> , <u>424/141.1</u> , <u>424/150.1</u> , <u>424/164.1</u> , <u>435/329</u> , <u>435/332</u> , <u>435/340</u> , <u>530/350</u> , <u>530/388.2</u> , <u>530/388.4</u>		
INT-CL: [07] <u>C07 K 16/00</u> , <u>C12 P 21/08</u>		

L5: Entry 4 of 10	File: USPT	Aug 21, 2001
US-PAT-NO: 6277379 DOCUMENT-IDENTIFIER: US 6277379 B1		
TITLE: Use of purified invaplex from gram negative bacteria as a vaccine		
DATE-ISSUED: August 21, 2001		
US-CL-CURRENT: <u>424/197.11</u> ; <u>424/193.1</u> , <u>424/203.1</u> , <u>424/234.1</u> , <u>424/241.1</u> , <u>424/249.1</u> , <u>424/252.1</u> , <u>424/258.1</u> , <u>435/975</u> , <u>530/350</u> , <u>536/123.1</u>		

INT-CL: [07] A61 K 39/385

L5: Entry 5 of 10

File: USPT

Jun 12, 2001

US-PAT-NO: 6245892

DOCUMENT-IDENTIFIER: US 6245892 B1

TITLE: Invaplex from gram negative bacteria, method of purification and methods of use

DATE-ISSUED: June 12, 2001

US-CL-CURRENT: 530/350; 424/282.1, 435/7.2, 530/416

INT-CL: [07] C07 K 14/00, C07 K 1/00, G01 N 33/53, A61 K 45/00

L5: Entry 6 of 10

File: USPT

Jul 4, 2000

US-PAT-NO: 6083683

DOCUMENT-IDENTIFIER: US 6083683 A

TITLE: Methods for detecting shigella bacteria or antibodies to shigella bacteria with an immunoassay

DATE-ISSUED: July 4, 2000

US-CL-CURRENT: 435/4; 424/282.1, 424/93.4, 435/252.1, 435/29, 435/34, 435/822, 435/975

INT-CL: [07] C12 Q 1/00

L5: Entry 7 of 10

File: DWPI

Dec 3, 2002

DERWENT-ACC-NO: 2003-129359

ABSTRACTED-PUB-NO: WO 200294190A

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TITLE: Inducing in a subject a protective immune response against infection with a first invasive gram-negative bacteria by administering a composition comprising Invaplex 50 from a second heterologous invasive gram negative bacteria

INT-CL (IPC): A61 K 0/00, A61 K 39/02, A61 K 39/108, A61 K 39/112, A61 K 39/116, A61 K 39/385, C07 K 1/00, G01 N 33/53

Derwent-CL (DC): B04, D16

CPI Codes: B04-B04C1; B04-C02V; B04-F10A; B04-F10A3; B04-F10A5; B04-N03; B14-A01A; B14-A01A3; B14-A01A5; B14-S11B; D05-H07;

L5: Entry 8 of 10

File: DWPI

Aug 25, 2004

DERWENT-ACC-NO: 2000-292989

ABSTRACTED-PUB-NO: US 6277379B

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TITLE: New vaccine for protection against infection with gram-negative bacteria comprising Invaplex of the bacteria to elicit protective antibodies

INT-CL (IPC): A61 K 0/00, A61 K 39/02, A61 K 39/385, A61 P 31/04

Derwent-CL (DC): B04, D16

CPI Codes: B04-B04M; B04-F10A; B04-G07; B11-C06; B14-A01A; B14-S11B; D05-H07; D05-H11;

L5: Entry 9 of 10

File: DWPI

Jan 20, 2004

DERWENT-ACC-NO: 2000-292988

ABSTRACTED-PUB-NO: US 6245892B

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TITLE: New composition comprising isolated Invaplex of gram-negative bacteria comprising at least one invasin protein associated with LPS of the gram-negative bacteria

INT-CL (IPC): A61 K 0/00, A61 K 45/00, C07 K 1/00, C07 K 14/00, C07 K 14/24, C07 K 16/00, C12 N 9/14, C12 P 21/08, G01 N 33/53

Derwent-CL (DC): B04, D16

CPI Codes: B04-B04L; B04-B04M; B04-F01; B04-F10A; B04-N03; D05-H04; D05-H07; D05-H09; D05-H11;

L5: Entry 10 of 10

File: DWPI

Apr 7, 2003

DERWENT-ACC-NO: 1996-209840

ABSTRACTED-PUB-NO: US 5679564A

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TITLE: Prodn. of enhanced antigenic enteric bacteria for use in e.g. vaccines - uses bile acids, bile salts, oxygen, nitrogen, carbon-di:oxide and divalent cation chelant 704283 B

INT-CL (IPC): A01 N 63/00, A61 K 39/00, A61 K 39/02, A61 K 39/106, A61 K 39/108, A61 K 39/38, A61 K 45/00, A61 P 1/00, A61 P 31/04, C12 N 0/00, C12 N 1/00, C12 N 1/12, C12 N 1/20, C12 N 1/38, C12 Q 1/00, C12 Q 1/02, C12 Q 1/04, G01 N 33/53, G01 N 33/531, G01 N 33/569, C12 N 1/20, C12 R 1:19, C12 N 1/20, C12 R 1:63, C12 N 1/20, C12 R 1:42, C12 N 1/20, C12 R 1:01, C12 N 1/20, C12 R 1:19, C12 N 1/20, C12 R 1:63, C12 N 1/20, C12 R 1:42, C12 N 1/20, C12 R 1:01

Derwent-CL (DC): B04, C07, D16, S03

CPI Codes: B04-F10A; C04-F10A; B04-G01; C04-G01; B10-B01B; C10-B01B; B11-C07A; C11-C07A; B12-K04A; C12-K04A; B14-S11B; C14-S11B; D05-H04; D05-H07; D05-H09;

EPI Codes: S03-E14H4;

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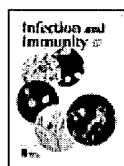
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Determination of the InvE Binding Site Required for Expression of IpaB of the *Shigella sonnei* Virulence Plasmid: Involvement of a ParB BoxA-Like Sequence

J. Bacteriol., September 1, 2003; 185(17): 5158 - 5165.

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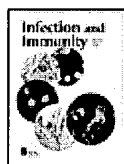
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Structural Characterization of the N Terminus of IpaC from *Shigella flexneri*

Infect. Immun., March 1, 2003; 71(3): 1255 - 1264.

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Identification of Substrates and Chaperone from the *Yersinia enterocolitica* 1B Ysa Type III Secretion System

Infect. Immun., January 1, 2003; 71(1): 242 - 253.

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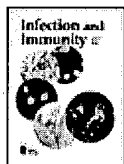
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S. M. Faruque, R. Khan, M. Kamruzzaman, S. Yamasaki, Q. S. Ahmad, T. Azim, G. B. Nair, Y. Takeda, and D. A. Sack

Isolation of *Shigella dysenteriae* Type 1 and *S. flexneri* Strains from Surface Waters in Bangladesh: Comparative Molecular Analysis of Environmental *Shigella* Isolates versus Clinical Strains

Appl. Envir. Microbiol., August 1, 2002; 68(8): 3908 - 3913.

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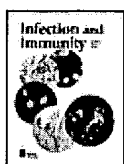
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M. M. Venkatesan, M. B. Goldberg, D. J. Rose, E. J. Grotbeck, V. Burland, and F. R. Blattner

Complete DNA Sequence and Analysis of the Large Virulence Plasmid of *Shigella flexneri*

Infect. Immun., May 1, 2001; 69(5): 3271 - 3285.

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***Shigella flexneri* IpaH7.8 Facilitates Escape of Virulent Bacteria from the Endocytic Vacuoles of Mouse and Human Macrophages**

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P J Jenks, F Megraud, and A Labigne

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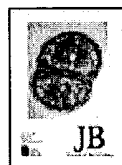
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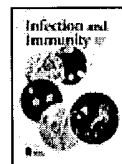
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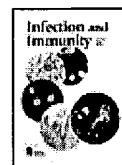
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